

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 26, 2005, 16:39:19 ; Search time 78.4963 Seconds
(without alignments)
282.715 Million cell updates/sec

Title: US-10-775-481A-2
Perfect score: 127
Sequence: 1 NNTFYCCLCCNPACAGCY 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US083 COMB.pcp.*
8: /cgn2_6/ptodata/1/paa/US084 COMB.pcp.*
9: /cgn2_6/ptodata/1/paa/US085 COMB.pcp.*
10: /cgn2_6/ptodata/1/paa/US086 COMB.pcp.*
11: /cgn2_6/ptodata/1/paa/US087 COMB.pcp.*
12: /cgn2_6/ptodata/1/paa/US088 COMB.pcp.*
13: /cgn2_6/ptodata/1/paa/US089 COMB.pcp.*
14: /cgn2_6/ptodata/1/paa/US090 COMB.pcp.*
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28: /cgn2_6/ptodata/1/paa/US102 COMB.pcp.*
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37: /cgn2_6/ptodata/1/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	19	1	PCT-US04-03765-2 Sequence 2, Appli
2	127	100.0	19	1	PCT-US94-12232-2 Sequence 2, Appli
3	127	100.0	19	8	US-08-468-449B-2 Sequence 2, Appli
4	127	100.0	19	16	US-09-263-477-2 Sequence 2, Appli
5	127	100.0	19	16	US-09-263-477A-2 Sequence 2, Appli
6	127	100.0	19	21	US-09-724-983-2 Sequence 2, Appli
7	127	100.0	19	32	US-10-621-684-2 Sequence 2, Appli
8	127	100.0	19	33	US-10-775-481A-2 Sequence 2, Appli
9	127	100.0	72	33	US-10-766-735-20 Sequence 20, Appli
10	127	100.0	72	33	US-10-796-719-20 Sequence 20, Appli
11	121	95.3	18	1	PCT-US04-03765-13 Sequence 13, Appli
12	121	95.3	18	1	PCT-US04-03765-38 Sequence 38, Appli
13	121	95.3	18	1	PCT-US94-12232-13 Sequence 13, Appli
14	121	95.3	18	1	PCT-US94-12232-38 Sequence 38, Appli
15	121	95.3	18	8	US-08-468-449B-13 Sequence 13, Appli
16	121	95.3	18	8	US-08-468-449B-38 Sequence 38, Appli
17	121	95.3	18	16	US-09-263-477-13 Sequence 13, Appli
18	121	95.3	18	16	US-09-263-477-38 Sequence 38, Appli
19	121	95.3	18	16	US-09-263-477A-13 Sequence 13, Appli
20	121	95.3	18	16	US-09-263-477A-38 Sequence 38, Appli
21	121	95.3	18	19	US-09-506-695-1 Sequence 1, Appli
22	121	95.3	18	19	US-09-506-695-8 Sequence 8, Appli
23	121	95.3	18	19	US-09-525-715-1 Sequence 1, Appli
24	121	95.3	18	21	US-09-724-983-13 Sequence 13, Appli
25	121	95.3	18	21	US-09-724-983-38 Sequence 38, Appli
26	121	95.3	18	32	US-10-621-684-13 Sequence 13, Appli
27	121	95.3	18	32	US-10-621-684-38 Sequence 38, Appli
28	121	95.3	18	33	US-10-766-735-2 Sequence 2, Appli
29	121	95.3	18	33	US-10-766-735-4 Sequence 4, Appli
30	121	95.3	18	33	US-10-775-481A-13 Sequence 13, Appli
31	121	95.3	18	33	US-10-775-481A-38 Sequence 38, Appli
32	121	95.3	18	33	US-10-796-719-2 Sequence 2, Appli
33	121	95.3	18	33	US-10-796-719-4 Sequence 4, Appli
34	120	94.5	18	1	PCT-US04-03765-7 Sequence 7, Appli
35	120	94.5	18	1	PCT-US94-12232-7 Sequence 7, Appli
36	120	94.5	18	8	US-08-468-449B-7 Sequence 7, Appli
37	120	94.5	18	16	US-09-263-477-7 Sequence 7, Appli
38	120	94.5	18	16	US-09-263-477A-7 Sequence 7, Appli
39	120	94.5	18	21	US-09-724-983-7 Sequence 7, Appli
40	120	94.5	18	32	US-10-621-684-7 Sequence 7, Appli
41	120	94.5	18	33	US-10-775-481A-7 Sequence 7, Appli
42	117	92.1	18	19	US-09-506-695-2 Sequence 2, Appli
43	117	92.1	18	19	US-09-506-695-18 Sequence 18, Appli
44	117	92.1	18	19	US-09-506-695-19 Sequence 19, Appli
45	116	91.3	18	19	US-09-506-695-15 Sequence 15, Appli

ALIGNMENTS

RESULT 1
PCT-US04-03765-2
; Sequence 2, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use of GCC Ligands
; FILE REFERENCE: 08321-168 PCI
; CURRENT FILING DATE: 2004-02-10
; PCT/US04/03765
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

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/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: ST Ia
PCT-US04-03765-2

Query Match      100.0%; Score 127; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NNTFYCCELCCNPACAGCY 19
Db      1 NNTFYCCELCCNPACAGCY 19

RESULT 2
PCT-US94-12232-2
/ Sequence 2, Application PC/TUS9412232
/ GENERAL INFORMATION:
/ APPLICANT: Waldman, Scott A.
/ TITLE OF INVENTION: Compositions That Specifically
/ TITLE OF INVENTION: Bind To Colorectal Cancer Cells
/ TITLE OF INVENTION: And Methods Of Using The Same
/ NUMBER OF SEQUENCES: 54
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
/ ADDRESSEE: Norris
/ STREET: One Liberty Place, 46th Floor
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/12232
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/141,892
/ FILING DATE: 26-OCT-1993
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/305,056
/ FILING DATE: 13-SEP-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-1360
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
PCT-US94-12232-2

Query Match      100.0%; Score 127; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NNTFYCCELCCNPACAGCY 19
Db      1 NNTFYCCELCCNPACAGCY 19

RESULT 3
US-08-468-449B-2
/ Sequence 2, Application US/08468449B
/ GENERAL INFORMATION:
/ APPLICANT: Waldman, Scott A.
/ TITLE OF INVENTION: ST Receptor Binding Compounds And Methods Of Using The Same
/ FILE REFERENCE: TJU-1588
/ CURRENT APPLICATION NUMBER: US/08/468,449B
/ CURRENT FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: 08/141,892
/ PRIOR FILING DATE: 1993-10-26
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Novel Sequence
US-08-468-449B-2

Query Match      100.0%; Score 127; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NNTFYCCELCCNPACAGCY 19
Db      1 NNTFYCCELCCNPACAGCY 19

RESULT 4
US-09-263-477-2
/ Sequence 2, Application US/09263477
/ GENERAL INFORMATION:
/ APPLICANT: Waldman, Scott A.
/ TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
/ TITLE OF INVENTION: of Using the Same
/ NUMBER OF SEQUENCES: 54
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch disk, 720 Kb
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/263,477
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/141,892
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-0903
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-263-477-2
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Query Match      100.0%; Score 127; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NNTFYCCCLCCNPACAGCY 19
Db      1 NNTFYCCCLCCNPACAGCY 19

RESULT 5
US-09-263-477A-2
; Sequence 2, Application US/09263477A
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,477A
; FILING DATE: 05-Mar-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-263-477A-2

Query Match      100.0%; Score 127; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NNTFYCCCLCCNPACAGCY 19
Db      1 NNTFYCCCLCCNPACAGCY 19

RESULT 6
US-09-724-983-2
; Sequence 2, Application US/09724983
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
; FILE REFERENCE: TJU-2444
; CURRENT APPLICATION NUMBER: US/09/724,983
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/468,449
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; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-724-983-2

Query Match      100.0%; Score 127; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NNTFYCCCLCCNPACAGCY 19
Db      1 NNTFYCCCLCCNPACAGCY 19

RESULT 7
US-10-621-684-2
; Sequence 2, Application US/10621684
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-621-684-2

Query Match      100.0%; Score 127; DB 32; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NNTFYCCCLCCNPACAGCY 19
Db      1 NNTFYCCCLCCNPACAGCY 19

RESULT 8
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US-10-775-481A-2
; Sequence 2, Application US/10775481A
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use of GCC Ligands
; FILE REFERENCE: 08321-0168 US1
; CURRENT APPLICATION NUMBER: US/10/775,481A
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: heat stable toxin peptide Ia
US-10-775-481A-2

Query Match 100.0%; Score 127; DB 33; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGCY 19
Db 1 NNTFYCCCLCCNPACAGCY 19

RESULT 9
US-10-766-735-20
; Sequence 20, Application US/10766735
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-039001
; CURRENT APPLICATION NUMBER: US/10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-766-735-20

Query Match 100.0%; Score 127; DB 33; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGCY 19
Db 54 NNTFYCCCLCCNPACAGCY 72

RESULT 10
US-10-796-719-20
; Sequence 20, Application US/10796719
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.

; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-20

Query Match 100.0%; Score 127; DB 33; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGCY 19
Db 54 NNTFYCCCLCCNPACAGCY 72

RESULT 11
PCT-US04-03765-13
; Sequence 13, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use of GCC Ligands
; FILE REFERENCE: 08321-168 PC1
; CURRENT APPLICATION NUMBER: PCT/US04/03765
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment
PCT-US04-03765-13

Query Match 95.3%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NNTFYCCCLCCNPACAGCY 19
Db 1 NNTFYCCCLCCNPACAGCY 18

RESULT 12
PCT-US04-03765-38
; Sequence 38, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason

APPLICANT: Schulz, Stephanie
APPLICANT: Wolfe, Henry R.
APPLICANT: Lubbe, Wilhelm
TITLE OF INVENTION: The Use Of GCC Ligands
FILE REFERENCE: 08321-168 PC1
CURRENT APPLICATION NUMBER: PCT/US04/03765
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 60/446,730
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: derivative
PCT-US04-03765-38

Query Match 95.3%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 13

PCT-US94-12232-13
Sequence 13, Application PC/TUS9412232

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12232
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-12232-13

Query Match 95.3%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 14

PCT-US94-12232-38
Sequence 38, Application PC/TUS9412232

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12232
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US94-12232-38

Query Match 95.3%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 15

US-08-468-449B-13

; Sequence 13, Application US/08468449B
; GENERAL INFORMATION:
; APPLICANT: Walzman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds And Methods Of Using The Same
; FILE REFERENCE: TJU-1588
; CURRENT APPLICATION NUMBER: US/08/468,449B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/141,892
; PRIOR FILING DATE: 1993-10-26
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-08-468-449B-13

Query Match 95.3%; Score 121; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCELCCNPACAGCY 19
| | | | | | | | | | | | | | | | | | | |
Db 1 NTFYCCELCCNPACAGCY 18

Search completed: March 26, 2005, 17:10:16
Job time : 79.4963 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:35:58 ; Search time 20.8029 Seconds
(without alignments)
353.241 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 127
Sequence: 1 NNTPYCCELCNCPACAGCY 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	19	2 AAR85946	Aar85946 ST Ia rec
2	127	100.0	19	2 AAY40508	Aay40508 ST recept
3	127	100.0	19	8 ADR45822	Adr45822 Amino aci
4	127	100.0	72	8 ADR48355	Adr48355 Immature
5	121	95.3	18	2 AAR85956	Aar85956 ST Ia rec
6	121	95.3	18	2 AAY40543	Aay40543 ST recept
7	121	95.3	18	2 AAY40518	Aay40518 ST recept
8	121	95.3	18	2 AAY02385	Aay02385 Heat stab
9	121	95.3	18	2 AAY29607	Aay29607 Escherich
10	121	95.3	18	2 AAY02397	Aay02397 Heat stab
11	121	95.3	18	8 ADR48330	Adr48330 E. coli S
12	121	95.3	18	8 ADR48332	Adr48332 C. freund
13	121	95.3	18	8 ADR48341	Adr48341 Bacterial
14	121	95.3	18	8 ADR45832	Adr45832 Amino aci
15	121	95.3	18	8 ADR45857	Adr45857 Amino aci
16	121	95.3	35	1 AAP30262	Aap30262 Sequence
17	120	94.5	18	2 AAR85950	Aar85950 ST Ia rec
18	120	94.5	18	2 AAY40512	Aay40512 ST recept
19	120	94.5	18	8 ADR45826	Adr45826 Amino aci
20	115	90.6	17	2 AAR85957	Aar85957 ST Ia' rec
21	115	90.6	17	2 AAY40519	Aay40519 ST recept
22	115	90.6	17	8 ADR45833	Adr45833 Amino aci
23	115	90.6	18	2 AAY06971	Aay06971 E. coli h
24	114	89.8	17	2 AAR85951	Aar85951 ST Ia rec
25	114	89.8	17	2 AAY40546	Aay40546 ST recept

26	114	89.8	17	2 AAY40513	Aay40513 ST recept
27	114	89.8	17	8 ADR45827	Adr45827 Amino aci
28	114	89.8	17	8 ADR45860	Adr45860 Amino aci
29	114	89.8	18	1 AAP40488	Aap40488 Sequence
30	113	89.0	18	2 AAR85982	Aar85982 ST I* rec
31	113	89.0	18	2 AAR85981	Aar85981 ST I* rec
32	113	89.0	18	2 AAY40545	Aay40545 ST recept
33	113	89.0	18	2 AAY40544	Aay40544 ST recept
34	113	89.0	18	8 ADR48342	Adr48342 Bacterial
35	113	89.0	18	8 ADR45859	Adr45859 Amino aci
36	113	89.0	18	8 ADR45858	Adr45858 Amino aci
37	112	88.2	36	1 AAP30263	Aap30263 Sequence
38	110	86.6	16	2 AAR85958	Aar85958 ST Ia rec
39	110	86.6	16	2 AAY40520	Aay40520 ST recept
40	110	86.6	16	8 ADR45834	Adr45834 Amino aci
41	108	85.0	16	2 AAR85952	Aar85952 ST Ia rec
42	108	85.0	16	2 AAY40514	Aay40514 ST recept
43	108	85.0	16	8 ADR45828	Adr45828 Amino aci
44	107	84.3	46	1 AAP50436	Aap50436 Network p
45	106	83.5	16	5 AAE28977	Aae28977 E. coli S

ALIGNMENTS

RESULT 1
AAR85946
ID AAR85946 standard; peptide; 19 AA.
AC AAR85946;
XX
DT 19-JAN-1996 (first entry)
XX
DE ST Ia receptor ligand portion.
XX
KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
KW colorectal; metastasis.
XX
OS Escherichia coli.
XX
PN WO9511694-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012232.
XX
PR 26-OCT-1993; 93US-00141892.
PR 13-SEP-1994; 94US-00305056.
XX
(UYJE-) UNIV JEFFERSON THOMAS.
Waldman SA;
XX
WPI; 1995-178646/23.
Conjugated cpds. which specifically bind to colorectal cancer cells -
comprise heat-stable toxin receptor binding moiety and active moiety
which may be a therapeutic agent or a radioactive agent.
Claim 3; Page 116; 133pp; English.

New conjugated compounds are provided which consist of (1) an ST receptor binding moiety and (2) an active moiety which is a radio- stable agent. 'ST' refers to a heat stable toxin produced by E.coli and other organisms. Especially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate

Sequence 19 AA;

XX DE XX

KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

XX Escherichia coli.

FN WO2004069165-A2.

XX 19-AUG-2004.

XX 28-JAN-2004; 2004WO-US002330.

XX 28-JAN-2003; 2003US-043098P.

PR 15-MAY-2003; 2003US-0471288P.

PR 12-NOV-2003; 2003US-0519460P.

XX (MICR-) MICROBIA INC.

XX Currie MG, Mahajan-Miklos S;

XX WPI; 2004-604332/58.

XX Novel purified peptide capable of activating the guanylate cyclase C

XX receptor, useful for treating obesity, congestive heart failure and

XX benign prostatic hyperplasia.

XX Disclosure; Page 30; 93pp; English.

CC The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis,
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasised or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

XX Sequence 72 AA;

Query Match 100.0%; Score 127; DB 8; Length 72;

Best Local Similarity 100.0%; Pred. No. 4.6e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NNTFYCCELCNCPACGY 19

Db 54 NNTFYCCELCNCPACGY 72

RESULT 5

AAAR85956

ID AAR85956 standard; peptide; 18 AA.

XX AAR85956;

XX 19-JAN-1996 (first entry)

XX ST Ia receptor ligand portion.

XX ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;

XX colorectal; metastasis.

XX Escherichia coli.

XX WO9511694-A1.

XX 04-MAY-1995.

XX 26-OCT-1994; 94WO-US012232.

XX 26-OCT-1993; 93US-00141892.

PR 13-SEP-1994; 94US-00305056.

XX (UWJE-) UNIV JEFFERSON THOMAS.

XX Waldman SA;

XX WPI; 1995-178646/23.

XX Conjugated cpds. which specifically bind to colorectal cancer cells -
 XX comprise heat-stable toxin receptor binding moiety and active moiety
 XX which may be a therapeutic agent or a radioactive agent.

XX Claim 3; Page 118; 133pp; English.

XX New conjugated compounds are provided which consist of (1) an ST receptor
 XX binding moiety and (2) an active moiety which is a radio-stable agent.
 XX 'ST' refers to a heat stable toxin produced by E.coli and other
 XX organisms. Especially the radiostable agent is a therapeutic agent (e.g.
 XX methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
 XX isotope) or nucleic acid; and the compound is used for the detection,
 XX imaging or treatment of colorectal tumours, particularly metastasised
 XX tumours. The present sequence is a specific example of an ST receptor
 XX binding peptide which can be used in the conjugate

XX Sequence 18 AA;

Query Match 95.3%; Score 121; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.8e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NNTFYCCELCNCPACGY 19

Db 1 NNTFYCCELCNCPACGY 18

RESULT 6

AAAY40543

ID AAY40543 standard; peptide; 18 AA.

XX AAY40543;

XX 03-DEC-1999 (first entry)

XX ST receptor binding peptide.

XX Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.

Oy

OS Escherichia coli.
XX
PN US5962220-A.
XX
XX 05-OCT-1999.
XX
XX 06-JUN-1995; 95US-00467920.
XX
XX 26-OCT-1993; 93US-00141892.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Waldman SA;
XX
XX WPI; 1999-571264/48.
XX
XX Conjugated compound comprising a receptor moiety and active moiety,
XX useful for the treatment/prevention of colorectal cancer.
XX
XX Claim 1; Col 35-36; 23pp; English.
XX
XX The invention relates to a conjugated compound that comprises a ST (heat-
XX stable toxin) receptor moiety selected from one of the sequences shown in
XX CC AAY40508-Y40559 and an active moiety (antisense molecule). The compound
XX CC is useful for the treatment of colorectal cancer. The use of the
XX CC conjugated compound is advantageous compared to antibodies since it binds
XX CC specifically to colorectal cells and has no toxic effect on normal cells
XX CC
XX SQ Sequence 18 AA;
XX
XX Query Match 95.3%; Score 121; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 NTFYCCCLCCNPACAGCY 19
XX DB 1 NTFYCCCLCCNPACAGCY 18
XX
XX RESULT 8
XX AAY02385
XX ID AAY02385 standard; peptide; 18 AA.
XX
XX XX
XX AC AAY02385;
XX
XX DT 09-JUL-1999 (first entry)
XX
XX DE Heat stable ST enterotoxin Sta.
XX
XX KW Selection; candidate drug; cell receptor binding; affinity;
XX biological receptor; rational drug design; combinatorial drug design;
XX KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
XX KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
XX
XX OS Escherichia coli.
XX
XX PN WO9909416-A2.
XX
XX PD 25-FEB-1999.
XX
XX PF 20-AUG-1998; 98WO-GB002504.
XX
XX PR 20-AUG-1997; 97GB-00017652.
XX
XX PA (NYCO-) NYCOMED IMAGING AS.
XX
XX PI (COCK/) COCKBAIN J.
XX
XX PI Wolfe HR;
XX
XX DR WPI; 1999-181156/15.
XX
XX PT Method of drug selection - and use of an acetamidomethyl-protected
XX polymer as a substrate in the solid state synthesis of an oligopeptide.
XX
XX PS Disclosure; Page 1; 38pp; English.
XX
XX CC The specification describes a method for selecting a candidate drug
XX compound having affinity for biological receptors. The method uses a
XX combination of rational and combinatorial drug design techniques. At
XX least 1 residue in the original cell receptor binding peptide is modified
XX to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
XX mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method
XX is used for identification of a candidate receptor antagonist or agonist.
XX CC The present peptide is a cell receptor binding peptide, and can thus be
XX used as a starting point for identification of candidate drug compounds,
XX using the method of the invention
XX
XX SQ Sequence 18 AA;
XX
XX Query Match 95.3%; Score 121; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 NTFYCCCLCCNPACAGCY 19
XX DB 1 NTFYCCCLCCNPACAGCY 18
XX
XX RESULT 7
XX AAY40518
XX ID AAY40518 standard; peptide; 18 AA.
XX
XX AC AAY40518;
XX
XX DT 03-DEC-1999 (first entry)
XX
XX DE ST receptor binding peptide.
XX
XX KW Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
XX
XX OS Escherichia coli.
XX
XX PN US5962220-A.
XX
XX PD 05-OCT-1999.
XX
XX PF 06-JUN-1995; 95US-00467920.
XX
XX PR 26-OCT-1993; 93US-00141892.
XX
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX XX Waldman SA;
XX
XX WPI; 1999-571264/48.
XX
XX PT Conjugated compound comprising a receptor moiety and active moiety,
XX useful for the treatment/prevention of colorectal cancer.
XX
XX PS Claim 1; Col 25-26; 23pp; English.
XX
XX XX The invention relates to a conjugated compound that comprises a ST (heat-

RESULT 10
AAY02397

KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

OS Escherichia coli.

XX WO2004069165-A2.

XX 19-AUG-2004.

XX 28-JAN-2004; 2004WO-US002390.

XX 28-JAN-2003; 2003US-0443098P.

XX 15-MAY-2003; 2003US-0471288P.

XX 12-NOV-2003; 2003US-0519460P.

XX (MICR-) MICROBIA INC.

XX Currie MG, Mahajan-Miklos S;

XX WPI; 2004-604332/58.

XX Novel purified peptide capable of activating the guanylate cyclase C

XX receptor, useful for treating obesity, congestive heart failure and

XX benign prostatic hyperplasia.

XX Disclosure; Page 28; 93pp; English.

XX The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inflammation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumors, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasis or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

XX Sequence 18 AA;

XX Query Match 95.3%; Score 121; DB 8; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 6.8e-07;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCELCCNPACAGCY 19

Db 1 NTFYCCELCCNPACAGCY 18

RESULT 12

ADR48332

ID ADR48332 standard; peptide; 18 AA.

XX ADR48332;

DT 04-NOV-2004 (first entry)

XX C. freundii ST peptide.

XX Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
 KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; virucide; immunosuppressive; antiallergic;
 KW nephrotropic; hepatotropic; ophthalmological; tranquiliser; hypnotic; nootropic;
 KW antidiabetic; guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

XX Citrobacter freundii.

XX WO2004069165-A2.

XX 19-AUG-2004.

XX 28-JAN-2004; 2004WO-US002390.

XX 28-JAN-2003; 2003US-0443098P.

XX 15-MAY-2003; 2003US-0471288P.

XX 12-NOV-2003; 2003US-0519460P.

XX (MICR-) MICROBIA INC.

XX Currie MG, Mahajan-Miklos S;

XX WPI; 2004-604332/58.

XX Novel purified peptide capable of activating the guanylate cyclase C

XX receptor, useful for treating obesity, congestive heart failure and

XX benign prostatic hyperplasia.

XX Disclosure; Page 28; 93pp; English.

XX The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
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 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is

CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasised or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

XX Sequence 18 AA;
 SQ

Query Match 95.3%; Score 121; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
 Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 13
 ADR48341
 ID ADR48341 standard; peptide; 18 AA.
 XX AC ADR48341;
 XX DT 04-NOV-2004 (first entry)
 XX DE Bacterial ST peptide #2.
 XX KW Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
 KW anorectic; cardiovascular; cyostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic;
 KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
 KW antididiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
 KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

XX Escherichia coli.
 OS
 XX WO2004069165-A2.
 PN
 XX 19-AUG-2004.
 PD
 XX 28-JAN-2004; 2004WO-US002390.
 XX 28-JAN-2003; 2003US-0443098P.
 PR 15-MAY-2003; 2003US-0471288P.
 PR 12-NOV-2003; 2003US-0519460P.
 XX (MICR-) MICROBIA INC.
 PA
 XX Currie MG, Mahajan-Miklos S;
 PI
 XX WPI; 2004-604332/58.
 DR
 XX Novel purified peptide capable of activating the guanylate cyclase C
 PT receptor, useful for treating obesity, congestive heart failure and

PT benign prostatic hyperplasia.
 XX Disclosure; Page 29; 93pp; English.
 PS
 XX The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastroenteral disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasised or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

XX Sequence 18 AA;
 SQ

Query Match 95.3%; Score 121; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
 Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 14
 ADR45832
 ID ADR45832 standard; peptide; 18 AA.
 XX AC ADR45832;
 XX DT 18-NOV-2004 (first entry)
 XX DE Amino acid sequence of heat stable toxin ST Ia fragment.
 XX heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
 KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
 KW ST Ia.
 XX Unidentified.
 OS
 XX WO2004071436-A2.
 PN
 XX 26-AUG-2004.
 PD
 XX 10-FEB-2004; 2004WO-US003765.

XX 10-FEB-2003; 2003US-0446730P.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;
 XX WPI; 2004-615913/59.
 XX
 XX Increasing ST receptor molecules on the surface of a colorectal, gastric
 XX or esophageal cancer cell to treat these cancers comprises administering
 XX ST receptor ligand molecules that bind to ST receptors on the surface of
 XX the cancer cell.
 XX
 XX Claim 6; SEQ ID NO 13; 97pp; English.
 XX
 XX The specification describes a method for increasing the number of heat
 XX stable toxin (ST) receptor molecules on the surface of a metastasised
 XX colorectal cancer cell. The method comprises administering, by continuous
 XX infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
 XX per hour for at least 6 hours, where ST receptor ligand molecules bind to
 XX ST receptors on the surface of the cancer cell in the individual and the
 XX number of ST receptor molecules on the surface of the cancer cell is
 XX increased. Therapeutic compositions comprising components which target ST
 XX receptors can then be used to inhibit proliferation of the colorectal,
 XX gastric and oesophageal cells. This method may be used for treating
 XX individuals that have diseases that affect colorectal, gastric and
 XX oesophageal cells, including colorectal, gastric or oesophageal cancers.
 XX The present sequence represents a fragment of a ST designated ST Ia (see
 XX ADR45822), which is used as the ST receptor ligand in the method of the
 XX invention.
 XX
 XX Sequence 18 AA;
 XX
 XX Query Match 95.3%; Score 121; DB 8; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 6.8e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 NTFYCCCLCCNPACAGCY 19
 XX | | | | | | | | | | | | | | | | | |
 XX Db 1 NTFYCCCLCCNPACAGCY 18
 XX
 XX RESULT 15
 XX ADR45857
 XX ID ADR45857 standard; peptide; 18 AA.
 XX AC ADR45857;
 XX DT 18-NOV-2004 (first entry)
 XX DE
 XX DE Amino acid sequence of a derivative of ST inhibitory peptide ST I*.
 XX heat stable toxin; ST: ST receptor; colorectal cancer; gastric cancer;
 XX oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
 XX ST I*.
 XX OS Unidentified.
 XX PN WO2004071436-A2.
 XX PD 26-AUG-2004.
 XX
 XX 10-FEB-2004; 2004WO-US003765.
 XX 10-FEB-2003; 2003US-0446730P.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;
 XX WPI; 2004-615913/59.

PT Increasing ST receptor molecules on the surface of a colorectal, gastric
 PT or esophageal cancer cell to treat these cancers comprises administering
 PT ST receptor ligand molecules that bind to ST receptors on the surface of
 PT the cancer cell.
 XX
 XX Claim 6; SEQ ID NO 38; 97pp; English.
 XX
 XX The specification describes a method for increasing the number of heat
 XX stable toxin (ST) receptor molecules on the surface of a metastasised
 XX colorectal cancer cell. The method comprises administering, by continuous
 XX infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
 XX per hour for at least 6 hours, where ST receptor ligand molecules bind to
 XX ST receptors on the surface of the cancer cell in the individual and the
 XX number of ST receptor molecules on the surface of the cancer cell is
 XX increased. Therapeutic compositions comprising components which target ST
 XX receptors can then be used to inhibit proliferation of the colorectal,
 XX gastric and oesophageal cells. This method may be used for treating
 XX individuals that have diseases that affect colorectal, gastric and
 XX oesophageal cells, including colorectal, gastric or oesophageal cancers.
 XX The present sequence represents a derivative of a ST inhibitory peptide
 XX designated ST I* (see ADR45823), which is used as the ST receptor ligand
 XX in the method of the invention.
 XX
 XX Sequence 18 AA;
 XX
 XX Query Match 95.3%; Score 121; DB 8; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 6.8e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 NTFYCCCLCCNPACAGCY 19
 XX | | | | | | | | | | | | | | | | | |
 XX Db 1 NTFYCCCLCCNPACAGCY 18

Search completed: March 26, 2005, 15:44:26
 Job time : 24.8029 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:38:19 ; Search time 5.68613 Seconds
(without alignments)
249.437 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 127

Sequence: 1 NNTFYCCCLCCNPACAGCY 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	19	1 US-08-141-892A-2	Sequence 2, Appli
2	127	100.0	19	2 US-08-583-447A-2	Sequence 2, Appli
3	127	100.0	19	3 US-08-467-920-2	Sequence 2, Appli
4	127	100.0	19	3 US-08-635-930-2	Sequence 2, Appli
5	127	100.0	19	3 US-09-193-997-2	Sequence 2, Appli
6	127	100.0	19	3 US-09-138-237A-2	Sequence 2, Appli
7	121	95.3	18	1 US-08-141-892A-13	Sequence 13, Appl
8	121	95.3	18	1 US-08-141-892A-38	Sequence 38, Appl
9	121	95.3	18	2 US-08-583-447A-13	Sequence 13, Appl
10	121	95.3	18	2 US-08-583-447A-38	Sequence 38, Appl
11	121	95.3	18	2 US-08-467-920-13	Sequence 13, Appl
12	121	95.3	18	2 US-08-467-920-38	Sequence 38, Appl
13	121	95.3	18	3 US-08-635-930-13	Sequence 13, Appl
14	121	95.3	18	3 US-08-635-930-38	Sequence 38, Appl
15	121	95.3	18	3 US-09-193-997-13	Sequence 13, Appl
16	121	95.3	18	3 US-09-193-997-38	Sequence 38, Appl
17	121	95.3	18	3 US-09-138-237A-13	Sequence 13, Appl
18	121	95.3	18	3 US-09-138-237A-38	Sequence 38, Appl
19	120	94.5	18	1 US-08-141-892A-7	Sequence 7, Appli
20	120	94.5	18	2 US-08-583-447A-7	Sequence 7, Appli
21	120	94.5	18	2 US-08-467-920-7	Sequence 7, Appli
22	120	94.5	18	3 US-08-635-930-7	Sequence 7, Appli
23	120	94.5	18	3 US-09-193-997-7	Sequence 7, Appli
24	120	94.5	18	3 US-09-138-237A-7	Sequence 7, Appli
25	115	90.6	17	1 US-08-141-892A-14	Sequence 14, Appl
26	115	90.6	17	2 US-08-583-447A-14	Sequence 14, Appl
27	115	90.6	17	2 US-08-467-920-14	Sequence 14, Appl

28	115	90.6	17	3 US-08-635-930-14	Sequence 14, Appl
29	115	90.6	17	3 US-09-193-997-14	Sequence 14, Appl
30	115	90.6	17	3 US-09-138-237A-14	Sequence 14, Appl
31	114	89.8	17	1 US-08-141-892A-8	Sequence 8, Appli
32	114	89.8	17	1 US-08-141-892A-41	Sequence 41, Appl
33	114	89.8	17	2 US-08-583-447A-8	Sequence 8, Appl
34	114	89.8	17	2 US-08-583-447A-41	Sequence 41, Appl
35	114	89.8	17	2 US-08-467-920-8	Sequence 8, Appl
36	114	89.8	17	2 US-08-467-920-41	Sequence 41, Appl
37	114	89.8	17	3 US-08-635-930-8	Sequence 8, Appli
38	114	89.8	17	3 US-08-635-930-41	Sequence 41, Appl
39	114	89.8	17	3 US-09-193-997-8	Sequence 8, Appli
40	114	89.8	17	3 US-09-193-997-41	Sequence 41, Appl
41	114	89.8	17	3 US-09-138-237A-8	Sequence 8, Appli
42	114	89.8	17	3 US-09-138-237A-41	Sequence 41, Appl
43	113	89.0	18	1 US-08-141-892A-39	Sequence 39, Appl
44	113	89.0	18	1 US-08-141-892A-40	Sequence 40, Appl
45	113	89.0	18	2 US-08-583-447A-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1

US-08-141-892A-2

; Sequence 2, Application US/08141892A

; Patent No. 5518888

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: St Receptor Binding Compounds and Methods

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888Bris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 720 Kb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/141,892A

; FILING DATE: 26-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: DeLuca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-0903

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-141-892A-2

Query Match 100.0%; Score 127; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.5e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGCY 19

|||||

Db 1 NNTFYCCCLCCNPACAGCY 19

|||||

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-920-2

Query Match 100.0%; Score 127; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0;

QY 1 NNTFYCCELCCNPACAGY 19
Db 1 NNTFYCCELCCNPACAGY 19

RESULT 4
US-08-635-930-2
; Sequence 2, Application US/08635930
; Patent No. 6060037
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: Wordperfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark

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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-635-930-2

Query Match 100.0%; Score 127; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGY 19
Db 1 NNTFYCCCLCCNPACAGY 19

RESULT 5
US-09-193-997-2
Sequence 2, Application US/09193997
Patent No. 6087109
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 6087109ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-193-997-2

Query Match 100.0%; Score 127; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGY 19

Db 1 NNTFYCCCLCCNPACAGY 19
RESULT 6
US-09-138-237A-2
Sequence 2, Application US/09138237A
Patent No. 6268159
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,237A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-138-237A-2

Query Match 100.0%; Score 127; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGY 19
Db 1 NNTFYCCCLCCNPACAGY 19

RESULT 7
US-08-141-892A-13
Sequence 13, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-141-892A-13

Query Match 95.3%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
DB 1 NTFYCCCLCCNPACAGCY 18

RESULT 8
US-08-141-892A-38
Sequence 38, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-141-892A-38

Query Match 95.3%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
DB 1 NTFYCCCLCCNPACAGCY 18

RESULT 9
US-08-583-447A-13
Sequence 13, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-583-447A-13

Query Match 95.3%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
DB 1 NTFYCCCLCCNPACAGCY 18

RESULT 10
US-08-583-447A-38
Sequence 38, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.

;; TITLE OF INVENTION: ST Receptor Binding Compounds and
;; TITLE OF INVENTION: Methods of Using the Same
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
;; STREET: One Liberty Place, 46th Floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: WordPerfect 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/583,447A
;; FILING DATE: 05-JAN-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/141,892
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1702
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-583-447A-38

Query Match 95.3%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
|||
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 11
US-08-467-920-13
;; Sequence 13, Application US/08467920
;; Patent No. 5962220
;; GENERAL INFORMATION:
;; APPLICANT: Waldman, Scott A.
;; TITLE OF INVENTION: Compositions That Specifically
;; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
;; TITLE OF INVENTION: And Methods Of Using The Same
;; NUMBER OF SEQUENCES: 54
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
;; ADDRESSEE: No. 596220ris
;; STREET: One Liberty Place, 46th Floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/467,920
;; FILING DATE:

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/141,892
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1589
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-467-920-13

Query Match 95.3%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
|||
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 12
US-08-467-920-38
;; Sequence 38, Application US/08467920
;; Patent No. 5962220
;; GENERAL INFORMATION:
;; APPLICANT: Waldman, Scott A.
;; TITLE OF INVENTION: Compositions That Specifically
;; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
;; TITLE OF INVENTION: And Methods Of Using The Same
;; NUMBER OF SEQUENCES: 54
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
;; ADDRESSEE: No. 596220ris
;; STREET: One Liberty Place, 46th Floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/467,920
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/141,892
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1589
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide

US-08-467-920-38

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 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
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 Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 13

US-08-635-930-13
 ; Sequence 13, Application US/08635930
 ; Patent No. 6060037

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.
 ; TITLE OF INVENTION: Compositions That Specifically Bind To
 ; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
 ; TITLE OF INVENTION: The Same
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
 ; STREET: One Liberty Place, 46th Floor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: WINDOWS 3.1
 ; SOFTWARE: WordPerfect 6.0/6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/635,930
 ; FILING DATE: 26-APR-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/141,892
 ; FILING DATE: 26-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/305,056
 ; FILING DATE: 13-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Deluca, Mark
 ; REGISTRATION NUMBER: 33,229
 ; REFERENCE/DOCKET NUMBER: TJU-1360

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-635-930-13

Query Match 95.3%; Score 121; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
 |||||

Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 14

US-08-635-930-38

; Sequence 38, Application US/08635930
 ; Patent No. 6060037

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.
 ; TITLE OF INVENTION: Compositions That Specifically Bind To
 ; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
 ; TITLE OF INVENTION: The Same
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
 ; STREET: One Liberty Place, 46th Floor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19103

; COMPUTER READABLE FORM:

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; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: WINDOWS 3.1

; SOFTWARE: WordPerfect 6.0/6.1

; CURRENT APPLICATION DATA:

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; FILING DATE: 26-APR-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/141,892

; FILING DATE: 26-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/305,056

; FILING DATE: 13-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-1360

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-635-930-38

Query Match 95.3%; Score 121; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NTFYCCCLCCNPACAGCY 19
 |||||

Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 15

US-09-193-997-13

; Sequence 13, Application US/09193997
 ; Patent No. 6087109

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.
 ; TITLE OF INVENTION: Compositions That Specifically
 ; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
 ; TITLE OF INVENTION: And Methods Of Using The Same
 ; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESS: No. 6087109ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,920
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-193-997-13

Query Match 95.3%; Score 121; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NTFYCCELCNCPACAGCY 19
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Db 1 NTFYCCELCNCPACAGCY 18

Search completed: March 26, 2005, 16:51:11
Job time : 5.68613 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:48:40 ; Search time 18.9307 Seconds
(without alignments)
332.314 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 127

Sequence: 1 NNTFYCELCCNPACAGY 19

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Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	127	100.0	19	US-10-621-684-2	Sequence 2, Appli
2	127	100.0	72	US-10-796-719-20	Sequence 20, Appl
3	121	95.3	18	US-10-621-684-13	Sequence 13, Appl
4	121	95.3	18	US-10-621-684-38	Sequence 38, Appl
5	121	95.3	18	US-10-796-719-2	Sequence 2, Appli
6	121	95.3	18	US-10-796-719-4	Sequence 4, Appli
7	120	94.5	18	US-10-621-684-7	Sequence 7, Appli
8	115	90.6	17	US-10-621-684-14	Sequence 14, Appl
9	114	89.8	17	US-10-621-684-8	Sequence 8, Appli
10	114	89.8	17	US-10-621-684-41	Sequence 41, Appl
11	113	89.0	18	US-10-621-684-39	Sequence 39, Appl
12	113	89.0	18	US-10-621-684-40	Sequence 40, Appl
13	113	89.0	18	US-10-796-719-11	Sequence 11, Appl

14	110	86.6	16	15	US-10-621-684-15	Sequence 15, Appl
15	108	85.0	16	15	US-10-621-684-9	Sequence 9, Appli
16	106	83.5	17	15	US-10-621-684-18	Sequence 18, Appl
17	106	83.5	18	10	US-09-930-915A-289	Sequence 289, Appl
18	106	83.5	18	14	US-10-082-014-79	Sequence 79, Appl
19	106	83.5	18	14	US-10-372-076-80	Sequence 80, Appl
20	106	83.5	18	15	US-10-621-684-3	Sequence 3, Appli
21	106	83.5	18	16	US-10-806-006-289	Sequence 289, App
22	106	83.5	18	16	US-10-677-074-80	Sequence 80, Appl
23	106	83.5	18	16	US-10-805-913-289	Sequence 289, App
24	106	83.5	18	17	US-10-796-719-3	Sequence 3, Appli
25	105	82.7	19	14	US-10-107-814-23	Sequence 23, Appl
26	105	82.7	19	15	US-10-371-966-1	Sequence 1, Appli
27	105	82.7	19	17	US-10-796-719-1	Sequence 1, Appli
28	105	82.7	19	17	US-10-796-719-26	Sequence 26, Appl
29	105	82.7	19	17	US-10-479-606-7	Sequence 7, Appli
30	105	82.7	21	17	US-10-796-719-39	Sequence 39, Appl
31	105	82.7	72	17	US-10-796-719-21	Sequence 21, Appl
32	104	81.9	15	15	US-10-621-684-16	Sequence 16, Appl
33	104	81.9	15	15	US-10-621-684-42	Sequence 42, Appl
34	103	81.1	15	15	US-10-621-684-10	Sequence 10, Appl
35	103	81.1	19	15	US-10-621-684-5	Sequence 5, Appli
36	103	81.1	19	17	US-10-796-719-84	Sequence 84, Appl
37	103	81.1	19	17	US-10-796-719-86	Sequence 86, Appl
38	102	80.3	19	17	US-10-796-719-27	Sequence 27, Appl
39	102	80.3	19	17	US-10-796-719-92	Sequence 92, Appl
40	102	80.3	21	17	US-10-796-719-40	Sequence 40, Appl
41	101	79.5	19	15	US-10-371-966-2	Sequence 2, Appli
42	101	79.5	19	17	US-10-796-719-87	Sequence 87, Appl
43	101	79.5	21	17	US-10-796-719-41	Sequence 41, Appl
44	100	78.7	15	15	US-10-621-684-36	Sequence 36, Appl
45	100	78.7	16	15	US-10-621-684-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-621-684-2
; Sequence 2, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100

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;
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-621-684-2

Query Match      100.0%; Score 127; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NNTFYCCCLCCNPACAGCY 19
Db      1 NNTFYCCCLCCNPACAGCY 19

RESULT 2
US-10-796-719-20
; Sequence 20, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-20

Query Match      100.0%; Score 127; DB 17; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NNTFYCCCLCCNPACAGCY 19
Db      54 NNTFYCCCLCCNPACAGCY 72

RESULT 3
US-10-621-684-13
; Sequence 13, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
US-10-621-684-13
; Sequence 13, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-621-684-13

Query Match      95.3%; Score 121; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NTFYCCCLCCNPACAGCY 19
Db      1 NTFYCCCLCCNPACAGCY 18

RESULT 4
US-10-621-684-38
; Sequence 38, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-621-684-38

Query Match 95.3%; Score 121; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
| | | | | | | | | | | | | | | | | |
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 5

US-10-796-719-2
; Sequence 2, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:

; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-2

Query Match 95.3%; Score 121; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
| | | | | | | | | | | | | | | | | |
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 6

US-10-796-719-4
; Sequence 4, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:

; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Citrobacter freundii
US-10-796-719-4

Query Match 95.3%; Score 121; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
| | | | | | | | | | | | | | | | | |
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 7

US-10-621-684-7
; Sequence 7, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-621-684-7

Query Match 94.5%; Score 120; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCNPACAGC 18
| | | | | | | | | | | | | | | | | |

Db 1 NNTFYCCCLCCNPACGC 18

RESULT 8

US-10-621-684-14
; Sequence 14, Application US/10621684
; Publication No. US20040029182A1

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1iris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-621-684-14

Query Match 90.6%; Score 115; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TFYCCCLCCNPACGCY 19

Db 1 TFYCCCLCCNPACGCY 17

RESULT 9

US-10-621-684-8
; Sequence 8, Application US/10621684
; Publication No. US20040029182A1

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1iris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-621-684-8

Query Match 89.8%; Score 114; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACGC 18

Db 1 NTFYCCCLCCNPACGC 17

RESULT 10

US-10-621-684-41
; Sequence 41, Application US/10621684
; Publication No. US20040029182A1

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1iris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-621-684-41

Query Match 89.8%; Score 114; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACGC 18
Db 1 NTFYCCCLCCNPACGC 17

RESULT 11

US-10-621-684-39
Sequence 39, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-621-684-39

Query Match 89.0%; Score 113; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.5e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACGC 19

Db 1 NTFYCCCLCCNPACGC 18

RESULT 12

US-10-621-684-40
Sequence 40, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-621-684-40

Query Match 89.0%; Score 113; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.5e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACGC 19
Db 1 NTFYCCCLCCNPACGC 18

RESULT 13

US-10-796-719-11
Sequence 11, Application US/10796719
Publication No. US20050020811A1
GENERAL INFORMATION:
APPLICANT: Currie, Mark G.

APPLICANT: Mahajan-Miklos, Shalina
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF GASTROINTESTINAL DISORDERS
FILE REFERENCE: 14184-043001
CURRENT APPLICATION NUMBER: US/10/796,719
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US 10/766,735
PRIOR FILING DATE: 2004-01-28

;; PRIOR APPLICATION NUMBER: US 60/443,098
;; PRIOR FILING DATE: 2003-01-28
;; PRIOR APPLICATION NUMBER: US 60/471,288
;; PRIOR FILING DATE: 2003-05-15
;; PRIOR APPLICATION NUMBER: US 60/519,460
;; PRIOR FILING DATE: 2003-11-12
;; NUMBER OF SEQ ID NOS: 149
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Escherichia coli
US-10-796-719-11

Query Match 89.0%; Score 113; DB 17; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.5e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
Db 1 NTFYCCCLCCNPACAGCY 18

RESULT 14
US-10-621-684-15
; Sequence 15, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-10-621-684-15
Query Match 86.6%; Score 110; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FYCCCLCCNPACAGCY 19
Db 1 FYCCCLCCNPACAGCY 16
RESULT 15
US-10-621-684-9
; Sequence 9, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-621-684-9
Query Match 85.0%; Score 108; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TFYCCCLCCNPACAGC 18
Db 1 TFYCCCLCCNPACAGC 16

Search completed: March 26, 2005, 17:16:37
Job time : 19.9307 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:18 ; Search time 16.365 Seconds
(without alignments)
594.533 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 127

Sequence: 1 NNTFYCCELCNCPACAGCY 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	72	1	HST1_ECOLI
2	121	95.3	18	2	Q7M0U3
3	119	93.7	61	2	Q6VEG9
4	106	83.5	18	1	HSTB_ECOLI
5	105	82.7	61	2	Q6VEG8
6	105	82.7	72	1	HST2_ECOLI
7	105	82.7	72	1	HST3_ECOLI
8	104	81.9	61	2	Q6VEG7
9	91	71.7	71	1	HSTB_YEREN
10	89	70.1	66	1	HSTC_YEREN
11	88	69.3	72	1	HSTN_VIBCH
12	84	66.1	19	2	Q6VEG7
13	84	66.1	28	2	Q6VEG7
14	84	66.1	71	1	HSTN_VIBCH
15	84	66.1	78	1	HSTO_VIBCH
16	84	66.1	78	1	HSTO_VIBCH
17	82	64.6	17	2	Q6VEG8
18	82	64.6	18	2	Q6VEG8
19	75	59.1	66	2	Q6VEG8
20	73	57.5	78	2	Q6VEG8
21	62.5	49.2	186	2	Q6VEG8
22	62.5	49.2	191	2	Q6VEG8
23	62.5	49.2	195	2	Q6VEG8
24	61	48.0	105	2	Q6VEG8
25	58	45.7	106	1	GUAU_MOUSE
26	58	45.7	106	1	GUAU_MOUSE
27	58	45.7	106	2	Q6VEG8
28	58	45.7	107	2	Q6VEG8
29	58	45.7	108	2	Q6VEG8
30	58	45.7	108	2	Q6VEG8
31	58	45.7	109	1	GUAU_DIDMA

32	58	45.7	112	1	GUAU_HUMAN
33	58	45.7	113	1	GUAU_PIG
34	58	45.7	116	2	Q98TH9
35	58	45.7	167	2	Q9D122
36	57	44.9	111	1	GUAV_CAVPO
37	57	44.9	118	2	Q8WTI6
38	56.5	44.5	122	2	Q70149
39	56.5	44.5	122	2	Q9D629
40	56.5	44.5	136	2	Q9D718
41	56.5	44.5	820	2	Q9FFK8
42	56	44.1	690	2	Q95436
43	55.5	43.7	84	2	Q9XTY0
44	55.5	43.7	152	2	Q9XVX3
45	55.5	43.7	164	2	Q22048

ALIGNMENTS

RESULT 1
HST1_ECOLI STANDARD; PRT; 72 AA.
AC P01559; 047653;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Heat-stable enterotoxin ST-1A/ST-P precursor.
GN Name=stai;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSDON=TN1681;
RX MEDLINE=81054703; PubMed=6254008;
RA So M., McCarthy B.J.;
RT "Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stable (ST) toxin and its identification in enterotoxigenic Escherichia coli strains.";
RT Proc. Natl. Acad. Sci. U.S.A. 77:4011-4015(1980).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=042:K86:H37 / 18D / ETEC;
RX MEDLINE=90368614; PubMed=2203756;
RA Dallas W.S.;
RT "The heat-stable toxin I gene from Escherichia coli 18D.";
RL J. Bacteriol. 172:5490-5495(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=85249571; PubMed=2990268;
RX Sekizaki T., Akashi H., Terakado N.;
RT "Nucleotide sequences of the genes for Escherichia coli heat-stable enterotoxin I of bovine, avian, and porcine origins.";
RL Am. J. Vet. Res. 46:909-912(1985).
RN [4]
RP DISULFIDE BONDS.
RC MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
RX Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T., Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh) produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170(1987).
RN [5]
RP PROCESSING.
RC MEDLINE=90368584; PubMed=2203746;
RX Okamoto K., Takahara M.;
RT "Synthesis of Escherichia coli heat-stable enterotoxin STp as a pre-pro form and role of the pro sequence in secretion.";
RL J. Bacteriol. 172:5260-5265(1990).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (0.89 ANGSTROMS) OF 59-71.
RX MEDLINE=94312375; PubMed=8038153;

RA Sato T., Ozaki H., Kitagawa Y., Katsube Y., Shimonishi Y.;
 RT "Structural characteristics for biological activity of heat-stable
 RT enterotoxin produced by enterotoxigenic *Escherichia coli*: X-ray
 RT crystallography of weakly toxic and nontoxic analogs.";
 RL Biochemistry 33:8641-8650(1994).
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC -----
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 CC -----
 DR EMBL; V00612; CAA23883.1; -;
 DR EMBL; M58746; AAA62776.1; -;
 DR EMBL; M25607; AAA24653.1; -;
 DR PIR; A01822; QHEC1.
 DR PDB; 1ETL; X-ray; @=59-71.
 DR PDB; 1ETW; X-ray; @=-.
 DR PDB; 1ETN; X-ray; @=-.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW 3D-structure; Enterotoxin; Signal; Toxin; Transposable element.
 FT SIGNAL 1 19
 FT PROPEP 20 54 Heat-stable enterotoxin ST-1A/ST-P.
 FT PRETIDE 55 72
 FT DISULFID 59 64
 FT DISULFID 60 68
 FT DISULFID 63 71 G -> P (in Ref. 3).
 FT CONFLICT 70 70
 FT TURN 61 62
 FT TURN 66 67
 FT TURN 69 70
 FT TURN 69 70
 FT TURN 69 70
 SQ SEQUENCE 72 AA; 8075 MW; 9288B766B3988264 CRC64;
 Query Match 100.0%; Score 127; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 6.6e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNTFYCCCLCCNPACAGCY 19
 Db 54 NNTFYCCCLCCNPACAGCY 72
 RESULT 2
 Q7M0U3 PRELIMINARY; PRT; 18 AA.
 AC Q7M0U3;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Heat-stable enterotoxin ST-1a.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89108617; PubMed=2912902;
 RA Guarino A., Giannella R., Thompson M.R.;
 RT "Citrobacter freundii produces an 18-amino-acid heat-stable
 RT enterotoxin identical to the 18-amino-acid *Escherichia coli* heat-
 RT stable enterotoxin (ST 1a)".
 RL Infect. Immun. 57:649-652(1989).
 DR PIR; A60103; A60103.
 DR HSSP; P01559; 1ETN.

DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 SQ SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;
 Query Match 95.3%; Score 121; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NTFYCCCLCCNPACAGCY 19
 Db 1 NTFYCCCLCCNPACAGCY 18
 RESULT 3
 Q6VEG9 PRELIMINARY; PRT; 61 AA.
 AC Q6VEG9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heat-stable enterotoxin ST-1a (Fragment).
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F7682;
 RX PubMed=15364995;
 RA Reichl U., Youssef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
 RT "Real-time fluorescence PCR assays for detection and characterization
 RT of heat-labile I and heat-stable I enterotoxin genes from
 RT enterotoxigenic *Escherichia coli*.";
 RL J. Clin. Microbiol. 42:4092-4100(2004).
 DR EMBL; AV342057; RAQ92974.1; -;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 61 AA; 6927 MW; 646D4AE2F895D957 CRC64;
 Query Match 93.7%; Score 119; DB 2; Length 61;
 Best Local Similarity 94.7%; Pred. No. 5.9e-08;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNTFYCCCLCCNPACAGCY 19
 Db 43 NNTFYCCCLCCNPACAGCY 61
 RESULT 4
 HSTB_ECOLI
 ID HSTB_ECOLI STANDARD; PRT; 18 AA.
 AC P01560;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin ST-2 (ST-B).
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=O42:K96:H37 / 18D / ETEC;
 RX MEDLINE=81264141; PubMed=7021541;
 RA Chan S.-K., Giannella R.A.;
 RT "Amino acid sequence of heat-stable enterotoxin produced by
 RT *Escherichia coli* pathogenic for man.";

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RESULT 6
HST2_ECOLI
ID ID_HST2_ECOLI STANDARD; PRT; 72 AA.
AC Q47185;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin A2 precursor (STA2).
DE Name=sta2;
GN Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=89108616; PubMed=2643580;
RA Guzman-Verdugo L.M., Kuperstoch Y.M.;
RT Recognition of two, Enterotoxin A2, heat-stable enterotoxin allele
RT sequences and lack of biological effect of changing the carboxy-
RT terminal tyrosine to histidine."
RL Infect. Immun. 57:645-648(1989).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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EMBL; M18345; AAA23729.1; -
PIR; JS0292; QHECIB.
HSP; P01559; 1ETN.
InterPro; IPR001489; Enterotoxin_HS.
Pfam; PF02048; Enterotoxin_HS; 1.
PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 53 By similarity.
FT PEPTIDE 54 72 Heat-stable enterotoxin A2.
FT DISULFID 59 64 By similarity.
FT DISULFID 60 68 By similarity.
FT DISULFID 63 71 By similarity.
FT SEQUENCE 72 AA; 7895 MW; D87850306E06B260 CRC64;
SQ
Query Match 82.7%; Score 105; DB 1; Length 72;
Best Local Similarity 78.9%; Pred. No. 3.9e-06;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 NNTFYCCCLCCNPACAGCY 19
DB 54 NSSNYCCCLCCNPACTGCY 72
:::|||||
:::|||||
:::|||||

RESULT 7
HST3_ECOLI
ID ID_HST3_ECOLI STANDARD; PRT; 72 AA.
AC P07965; P26588;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin A3/A4 precursor (STA3/STA4) (ST-H).
DE Name=sta3; Synonyms=sta4;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
[1]

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DR EMBL; J03311; AAA24652.1; -
DR EMBL; M34916; AAA23990.1; -
DR EMBL; M18346; AAA23730.1; -
DR EMBL; M29255; AAA24686.1; -
DR PIR; JS0292; QHECIB.
DR PIR; JT0373; QHEC4.
DR HSPS; P01559; IFTN.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; ENTEROTOXIN_H_STABLE; 1.
KW PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
Direct protein sequencing; Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19
FT PROPEP 20 53
FT PEPTIDE 54 72      Heat-stable enterotoxin A3/A4.
FT DISULFID 59 64
FT DISULFID 60 68
FT DISULFID 63 71
FT CONFLICT 19 19      A -> P (in Ref. 2).
SQ SEQUENCE 72 AA; 7909 MW; ICSC9292BFCBA6BA CRC64;

Query Match          82.7%; Score 105; DB 1; Length 72;
Best Local Similarity 78.9%; Pred.No. 3.9e-06;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNTFYCCELCCNPACAGCY 19
DB 54 NSSNYCCELCCNPACTGCG 72

RESULT 8
Q6VEG7 PRELIMINARY; PRT; 61 AA.
AC Q6VEG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE DE Heat-stable enterotoxin ST Ib (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R544;
RX PubMed=15364995;
RA Reischl U., Yousef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
of heat-labile I and heat-stable I enterotoxin genes from
enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL; AY342059; AAQ92976.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
DR NON TER 1
SQ SEQUENCE 61 AA; 6556 MW; 89788D3FAB3DCA0A CRC64;

Query Match          81.9%; Score 104; DB 2; Length 61;
Best Local Similarity 78.9%; Pred.No. 4.6e-06;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNTFYCCELCCNPACAGCY 19
DB 43 NGSNYCCELCCNPACTGCG 61

RESULT 9
HSTB_YEREN STANDARD; PRT; 71 AA.
ID HSTB_YEREN
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AC P74977;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin B precursor (Y-S7B).
GN Name=yetB;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=84-50 / Serotype O:3;
RX MEDLINE=98008784; PubMed=9344780; DOI=10.1006/mpat.1997.0146;
RA Ramamurthy T., Yoshino K., Huang X., Nair G.B., Carniel E.,
RA Maruyama T., Fukushima H., Takeda T.;
RT "The novel heat-stable enterotoxin subtype gene (yetB) of Yersinia
RT enterocolitica: nucleotide sequence and distribution of the yet
RT genes.";
RL Microb. Pathog. 23:189-200(1997).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells. Could play an important role in pathogenesis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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DR EMBL; D88145; BAAL3544.1; -.
DR HSSP; P01559; 1ETN.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 52
FT CHAIN 53 71 Heat-stable enterotoxin B.
FT DISULFID 59 64 By similarity.
FT DISULFID 60 68 By similarity.
FT DISULFID 63 71 By similarity.
SQ SEQUENCE 71 AA; 7670 MW; ED69F61ACDD4F50 CRC64;

Query Match 71.7%; Score 91; DB 1; Length 71;
Best Local Similarity 76.5%; Pred. No. 0.0022;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NTFVCCCLCCNPACAGC 18
Db 55 NDDWCCEVCNCPACAGC 71

RESULT 10
HST_YERK
ID HST_YERK STANDARD; PRT; 66 AA.
AC P31518;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin precursor.
GN Name=yet;
OS Yersinia kristensenii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=28152;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP490 / Serotype O:12,25;

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RA Ibrahim A., Liesack W., Stackebrandt E.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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DR EMBL; X69218; CAA49152.1; -.
DR PIR; S31652; S31652.
DR HSSP; P01559; 1ETN.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Enterotoxin; Signal.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 50
FT CHAIN 51 66 Heat-stable enterotoxin (By similarity).
FT DISULFID 54 59 By similarity.
FT DISULFID 55 63 By similarity.
FT DISULFID 58 66 By similarity.
SQ SEQUENCE 66 AA; 7068 MW; 27BE7006675CC075 CRC64;

Query Match 70.1%; Score 89; DB 1; Length 66;
Best Local Similarity 85.7%; Pred. No. 0.00038;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YCCCLCCNPACAGC 18
Db 53 WCCEVCNCPACAGC 66

RESULT 11
HSTC_YEREN
ID HSTC_YEREN STANDARD; PRT; 72 AA.
AC O50319;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin C precursor (Y-STC).
GN Name=ystC;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-11;
RX MEDLINE=97202479; PubMed=9049998; DOI=10.1006/mpat.1996.0094;
RA Huang X., Yoshino K., Nakao H., Takeda T.;
RT "Nucleotide sequence of a gene encoding the novel Yersinia
RT enterocolitica heat-stable enterotoxin that includes a pro-region-like
RT sequence in its mature toxin molecule.";
RL Microb. Pathog. 22:89-97(1997).
RN [2]
RP SEQUENCE OF 20-72.
RC STRAIN=Serotype O:3;
RX MEDLINE=95246844; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
RA Yoshino K., Takao T., Huang X., Murata H., Nakao H., Takeda T.,
RA Shimonishi Y.;
RT "Characterization of a highly toxic, large molecular size heat-stable
RT enterotoxin produced by a clinical isolate of Yersinia
RT enterocolitica.";
RL FEBS Lett. 362:319-322(1995).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate

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cyclase and increases cyclic GMP levels within the host intestinal epithelial cells. Highly toxic.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.

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EMBL: D63578; BAA23656.1; -
 HSP: P01559; 1FTN
 InterPro: IPR001489; Enterotoxin HS.
 Pfam: PF02048; Enterotoxin HS; 1.
 PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
 FT SIGNAL 1 19
 CHAIN 20 72 Heat-stable enterotoxin C.
 DISULFID 60 65 By similarity.
 FT DISULFID 61 69 By similarity.
 FT DISULFID 64 72 By similarity.
 SQ SEQUENCE 72 AA; 7639 MW; 7C0D83893C2F981D CRC64;

Query Match 69.3%; Score 88; DB 1; Length 72;
 Best Local Similarity 72.2%; Pred. No. 0.00054;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNTFYCCELCNCPACGC 18
 Db 55 NDWDWCCELCNCPACGCG 72

RESULT 12

Q9R579 Q9R579 PRELIMINARY; PRT; 19 AA.
 AC Q9R579
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 01-ST-3-HEAT-stable enterotoxin.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
 RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
 RA Takeda T., Shimonishi Y.,
 RT "Purification and sequence determination of heat-stable enterotoxin
 RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
 RT O1.";
 RL FEBS Lett. 326:83-86(1993).
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001489; Enterotoxin HS.
 DR Pfam: PF02048; Enterotoxin HS; 1.
 DR PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
 SQ SEQUENCE 19 AA; 2048 MW; 308015F1A18D601C CRC64;

Query Match 66.1%; Score 84; DB 2; Length 19;
 Best Local Similarity 70.6%; Pred. No. 0.00057;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNTFYCCELCNCPACGC 18
 Db 1 NLIDCCEICNCPACGCG 17

RESULT 13

Q9R578 Q9R578 PRELIMINARY; PRT; 28 AA.
 AC Q9R578
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 01-ST-4-HEAT-stable enterotoxin.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
 RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
 RA Takeda T., Shimonishi Y.,
 RT "Purification and sequence determination of heat-stable enterotoxin
 RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
 RT O1.";
 RL FEBS Lett. 326:83-86(1993).
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001489; Enterotoxin HS.
 DR Pfam: PF02048; Enterotoxin HS; 1.
 DR PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
 SQ SEQUENCE 28 AA; 3080 MW; 25ECADAFEC57DB72 CRC64;

Query Match 66.1%; Score 84; DB 2; Length 28;
 Best Local Similarity 70.6%; Pred. No. 0.00079;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNTFYCCELCNCPACGC 18
 Db 10 NLIDCCEICNCPACGCG 26

RESULT 14

HSTA YEREN
 ID HSTA YEREN STANDARD; PRT; 71 AA.
 AC P07593;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin A precursor (YST-A).
 GN Name-ystA; Synonyms-yst;
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Serotype O:8;
 RX MEDLINE=93051243; PubMed=1427005; DOI=10.1016/0378-1097(92)90364-T;
 RA Ibrahim A., Liesack W., Pike S., Stackebrandt E.;
 RT "The polymerase chain reaction: an epidemiological tool to
 RT differentiate between two clusters of pathogenic Yersinia
 RT enterocolitica strains";
 RL FEMS Microbiol. Lett. 76:63-66(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W1024 / Serotype O:9;
 RX MEDLINE=90354067; PubMed=2201642;
 RA Delor I., Kaechenbeck A., Wauters G., Cornelis G.R.;
 RT "Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding
 RT the heat-stable enterotoxin, and prevalence of the gene among
 RT pathogenic and nonpathogenic yersiniae.";
 RL Infect. Immun. 58:2983-2988(1990).
 RN [3]
 RP SEQUENCE OF 54-71.
 RX MEDLINE=86004705; PubMed=4043080;
 RA Takao T., Tomimaga N., Yoshimura S., Shimonishi Y., Hara S., Inoue T.,
 RA Miyama A.;
 RT "Isolation, primary structure and synthesis of heat-stable enterotoxin

RT produced by Yersinia enterocolitica.";
 RL J. Biochem. 152:199-206(1985).
 CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- INDUCTION: In cultured cells, expressed only at temperatures <30
 CC degrees Celsius. Under conditions of high osmolality and alkaline
 CC pH (as it is the case in the host's intestine), it is expressed at
 CC 37 degrees Celsius.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC
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 CC
 CC EMBL; X65999; CAA46801.1; -;
 CC EMBL; U09235; AAA18472.1; -;
 CC PIR; S25659; S25659.
 CC HSP; P01559; 1ETN.
 CC InterPro; IPR001489; Enterotoxin_HS.
 CC Pfam; PF02048; Enterotoxin_HS; 1.
 CC PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 CC Direct protein sequencing; Enterotoxin; Signal; Toxin.
 CC SIGNAL 1 19 Potential.
 CC PROPEP 20 53
 CC CHAIN 54 71 Heat-stable enterotoxin A.
 CC DISULFID 59 64 By similarity.
 CC DISULFID 60 68 By similarity.
 CC DISULFID 63 71 By similarity.
 CC VARIANT 48 48 L->S
 CC SEQUENCE 71 AA; 7494 MW; 022F99B3800C861B CRC64;
 SQ
 Query Match 66.1%; Score 84; DB 1; Length 71;
 Best Local Similarity 84.6%; Pred. No. 0.0017;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 CCELCNCPACAGC 18
 Db 59 CCDVCCNPACAGC 71
 ||:|||||||
 ||:|||||||
 RESULT 15
 ID HSTN_VIBCH STANDARD; PRT; 78 AA.
 AC P04429;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin ST precursor (Nonagglutinating cholera vibrios
 DE ST) (NAG-ST) (Non O1-ST).
 GN Name=stn;
 OS Vibrio cholerae, and
 OS Vibrio mimicus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666, 674;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=V.cholerae; STRAIN=NRT36;
 RX MEDLINE=90382953; PubMed=2205577;
 RA Ogawa A., Kato J.I., Watanabe H., Nair B.G., Takeda T.;
 RT "Cloning and nucleotide sequence of a heat-stable enterotoxin gene
 RT from Vibrio cholerae non-O1 isolated from a patient with traveler's
 RT diarrhea.";
 RL Infect. Immun. 58:3325-3329(1990).
 RN [2]
 RP SEQUENCE OF 62-78.
 RC SPECIES=V.cholerae; STRAIN=Seroovar non-O1;

RX MEDLINE=86056320; PubMed=4065341; DOI=10.1016/0014-5793(85)80163-0;
 RA Takao T., Shimonishi Y., Kobayashi M., Nishimura O., Arita M.,
 RA Takeda T., Honda T., Miwatani T.;
 RT "Amino acid sequence of heat-stable enterotoxin produced by Vibrio
 RT cholerae non-O1";
 RL FEBS Lett. 193:250-254 (1985).
 RL [3]
 RN SEQUENCE OF 62-78.
 RC SPECIES=V.mimicus; STRAIN=AQ-0915;
 RX MEDLINE=91257548; PubMed=2044934; DOI=10.1016/0378-1097(91)90536-J;
 RA Arita M., Honda T., Miwatani T., Takeda T., Takao T., Shimonishi Y.;
 RT "Purification and characterization of a heat-stable enterotoxin of
 RT Vibrio mimicus";
 RL FEMS Microbiol. Lett. 63:105-110(1991).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC
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 CC
 CC EMBL; M85198; AAA64889.1; -;
 CC PIR; A41469; QHVCL.
 CC HSP; P01559; 1ETN.
 CC InterPro; IPR001489; Enterotoxin_HS.
 CC Pfam; PF02048; Enterotoxin_HS; 1.
 CC PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 CC Direct protein sequencing; Enterotoxin; Signal; Toxin.
 CC SIGNAL 1 18 Potential.
 CC PROPEP 19 61
 CC CHAIN 62 78 Heat-stable enterotoxin ST.
 CC DISULFID 64 69 By similarity.
 CC DISULFID 65 73 By similarity.
 CC DISULFID 68 76 By similarity.
 CC SEQUENCE 78 AA; 8830 MW; EED385B29BD0964F CRC64;
 SQ
 Query Match 66.1%; Score 84; DB 1; Length 78;
 Best Local Similarity 70.6%; Pred. No. 0.0019;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 NTFYCCCLCNCPACAGC 18
 Db 60 NLIDCCICCNPCAGC 76
 ||:|||||||
 ||:|||||||
 Search completed: March 26, 2005, 16:48:33
 Job time : 19.365 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:49 ; Search time 4.0219 Seconds
(without alignments)
454.541 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 127

Sequence: 1 NNTFYCCELCNPAAGCY 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	72	1 QHEC1	heat-stable entero
2	121	95.3	18	2 A60103	heat-stable entero
3	106	83.5	18	1 QHEC2	heat-stable entero
4	105	82.7	72	1 QHEC4	heat-stable entero
5	105	82.7	72	1 QHEC1B	heat-stable entero
6	89	70.1	66	2 S31652	enterotoxin - Yers
7	88	69.3	53	2 S68705	heat-stable entero
8	84	66.1	71	2 S25659	heat-stable entero
9	84	66.1	78	1 QHVC1	heat-stable entero
10	82	64.6	17	2 A54534	heat-stable entero
11	71	55.9	65	2 S34671	heat-stable entero
12	62.5	49.2	186	2 A45910	ultra-high-sulfur
13	58	45.7	112	2 JC4651	uroguanylin precur
14	58	45.7	116	2 JC7620	guanylin precursor
15	56.5	44.5	122	2 JC6548	high sulfur protei
16	55.5	43.7	84	2 T24385	hypothetical prote
17	55.5	43.7	152	2 T18975	hypothetical prote
18	55.5	43.7	168	2 T24272	hypothetical prote
19	55.5	43.7	188	2 T15651	hypothetical prote
20	54	42.5	56	1 WTEF	testis-specific pr
21	54	42.5	68	2 S25775	testis-specific pr
22	53	41.7	58	2 S25774	testis-specific pr
23	52.5	41.3	175	2 S37649	high-sulfur kerati
24	52.5	41.3	177	2 S37650	high-sulfur kerati
25	52	40.9	172	2 T17106	high-sulfur wool m
26	52	40.9	165	2 T52054	cellulose synthase
27	51.5	40.6	188	2 JC6547	high sulfur protei
28	51	40.2	152	1 KRSHHC	keratin high-sulfu
29	51	40.2	152	2 T47111	high-sulfur wool m

30	51	40.2	152	2	I47109	high-sulfur wool m
31	51	40.2	152	2	I47108	high-sulfur wool m
32	51	40.2	152	2	I47112	high-sulfur wool m
33	51	40.2	156	1	KRSHHB	keratin high-sulfu
34	51	40.2	162	2	I47107	high-sulfur wool m
35	51	40.2	172	1	KRSHHA	keratin high-sulfu
36	51	40.2	182	1	KRSHHD	keratin high-sulfu
37	51	40.2	182	2	I47105	high-sulfur wool m
38	50.5	39.8	61	2	A37425	metallothionein 2
39	50.5	39.8	62	2	S54336	metallothionein-2a
40	50.5	39.8	62	2	S54335	metallothionein-2c
41	50.5	39.8	151	2	S60314	hair keratin cyste
42	50.5	39.8	327	2	D71491	hypothetical prote
43	50.5	39.8	328	2	D81650	conserved hypother
44	50	39.4	96	2	T43470	hypothetical prote
45	50	39.4	115	1	A46279	guanylin precursor

ALIGNMENTS

RESULT 1

QHEC1

heat-stable enterotoxin ST-I precursor - Escherichia coli

N;Alternate names: heat-stable enterotoxin estAI

C;Species: Escherichia coli

C;Date: 31-Aug-1980 #sequence revision 31-Aug-1980 #text_change 09-Jul-2004

C;Accession: A01822; A30985; A36732; JT0374; I51932

R;SO, M.; McCarthy, B.J.

Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980

A;Title: Nucleotide sequence of the bacterial transposon Tn1691 encoding a heat-stable (S

A;Reference number: A01822; MUID:81054703; PMID:6254008

A;Accession: A01822

A;Molecule type: DNA

A;Residues: 1-72 <LAZ>

A;Cross-references: UNIPROT:P01559; GB:V00612; GB:J01831; NID:g43704; PIDN:CAA23883.1; P

R;Lazure, C.; Seidah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S.

Can. J. Biochem. Cell Biol. 61, 287-292, 1983

A;Title: Primary structure determination of Escherichia coli heat-stable enterotoxin of

A;Reference number: A30985; MUID:83284515; PMID:6349752

A;Accession: A30985

A;Molecule type: protein

A;Residues: 55-72 <LAZ2>

A;Experimental source: strain F11

R;Dallas, W.S.

J. Bacteriol. 172, 5490-5493, 1990

A;Title: The heat-stable toxin I gene from Escherichia coli 18D.

A;Reference number: A36732; MUID:90368614; PMID:2203756

A;Accession: A36732

A;Molecule type: DNA

A;Residues: 1-72 <DAL>

A;Cross-references: GB:M58746; NID:g145860; PIDN:AAA62776.1; PID:g145861

A;Experimental source: strain 18D

R;Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;

Plasmid 20, 42-53, 1988

A;Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri

A;Reference number: JT0373; MUID:89202548; PMID:3071819

A;Accession: JT0374

A;Molecule type: DNA

A;Residues: 1-72 <STI>

R;Sekizaki, T.; Akashi, H.; Terakado, N.

Am. J. Vet. Res. 46, 909-912, 1985

A;Title: Nucleotide sequences of the genes for Escherichia coli heat-stable enterotoxin

A;Reference number: I51932; MUID:85249571; PMID:2990268

A;Accession: I51932

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-69, 'p', 71-72 <RES>

A;Cross-references: GB:M25607; NID:g147877; PIDN:AAA24653.1; PID:g147878

C;Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic stra

ular sizes.

C;Superfamily: heat-stable enterotoxin ST

C;Keywords: enterotoxin; heat-stable protein

F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-54/Domain: propeptide #status predicted <PRO>
 F;55-72/Product: heat-stable enterotoxin ST-I #status experimental <MAT>
 F;59-64,60-68,63-71/Disulfide bonds: #status predicted

Query Match 100.0%; Score 127; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 5,4e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNTFYCCCLCCNPACAGCY 19
 Db 54 NNTFYCCCLCCNPACAGCY 72

RESULT 2
 A60103
 heat-stable enterotoxin ST-Ia - Citrobacter freundii
 C;Species: Citrobacter freundii
 C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
 C;Accession: A60103
 R;Guarino, A.; Giannella, R.; Thompson, M.R.
 Infect. Immun. 57, 649-652, 1989
 A;Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identical to enterotoxin ST-I
 A;Reference number: A60103; MUID:89108617; PMID:2912902
 A;Accession: A60103
 A;Molecule type: protein
 A;Residues: 1-18 <GUA>
 A;Cross-references: UNIPROT:Q7M0U3
 C;Superfamily: heat-stable enterotoxin ST

Query Match 95.3%; Score 121; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1,1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNTFYCCCLCCNPACAGCY 19
 Db 1 NNTFYCCCLCCNPACAGCY 18

RESULT 3
 QHEC2
 heat-stable enterotoxin ST-2 - Escherichia coli
 C;Species: Escherichia coli
 C;Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
 C;Accession: A01823
 R;Chan, S.K.; Giannella, R.A.
 J. Biol. Chem. 256, 7744-7746, 1981
 A;Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pathogenic strain 8639
 A;Reference number: A01823; MUID:81264141; PMID:7021541
 A;Accession: A01823
 A;Molecule type: protein
 A;Residues: 1-18 <CHA>
 A;Cross-references: UNIPROT:P01560
 A;Experimental source: strain 18D, serotype 0.42:k86:H37
 C;Comment: This enterotoxin is one of several, of differing molecular sizes, produced by isolates of the heat-stable enterotoxin ST-I.
 C;Superfamily: heat-stable enterotoxin ST
 C;Keywords: enterotoxin; heat-stable protein
 F;1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
 F;5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 83.5%; Score 106; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 5,4e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNTFYCCCLCCNPACAGC 18
 Db 1 NNTFYCCCLCCNPACAGC 17

RESULT 4
 QHEC4
 heat-stable enterotoxin ST-A4 precursor - Escherichia coli

C;Species: Escherichia coli
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: J03073; A35978
 R;Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Plasmid 20, 42-53, 1988
 A;Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escherichia coli heat-stable enterotoxin ST-A4 precursor
 A;Reference number: J03073; MUID:89202548; PMID:3071819
 A;Accession: J03073
 A;Molecule type: DNA
 A;Residues: 1-72 <STI>
 A;Cross-references: UNIPROT:P07965; GB:J03311; NID:g147875; PIDN:AAA24652.1; PID:g147876
 R;Zhou, X.; Shen, L.P.; Chi, C.W.
 Toxicon 28, 453-456, 1990
 A;Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stable enterotoxin ST-A4 precursor
 A;Reference number: A35978; MUID:90273381; PMID:2190361
 A;Accession: A35978
 A;Molecule type: DNA
 A;Residues: 1-72 <ZHO>
 C;Genetics:
 A;Gene: estA4
 C;Superfamily: heat-stable enterotoxin ST
 C;Keywords: enterotoxin; heat-stable protein
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-53/Domain: propeptide #status predicted <PRO>
 F;54-72/Product: heat-stable enterotoxin #status predicted <MAT>
 F;59-64,60-68,63-71/Disulfide bonds: #status predicted

Query Match 82.7%; Score 105; DB 1; Length 72;
 Best Local Similarity 78.9%; Pred. No. 1,6e-05;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNTFYCCCLCCNPACAGCY 19
 Db 54 NNTFYCCCLCCNPACAGCY 72

RESULT 5
 QHEC1B
 heat-stable enterotoxin ST-Ib precursor - Escherichia coli
 N;Alternate names: heat-stable enterotoxin ST-A2
 C;Species: Escherichia coli
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C;Accession: J02092; A33068; A33067; A30567
 R;Moseley, S.L.; Hardy, J.W.; Hug, M.I.; Echeverria, P.; Falkow, S.
 Infect. Immun. 39, 1167-1174, 1983
 A;Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stable enterotoxin ST-Ib precursor
 A;Reference number: J02092; MUID:83184648; PMID:6341230
 A;Accession: J02092
 A;Molecule type: DNA
 A;Residues: 1-72 <MOS>
 A;Cross-references: UNIPROT:Q47185; UNIPROT:P07965; GB:M34916; NID:g146407; PIDN:AAA23990
 R;Dwarkanath, P.; Visweswariah, S.S.; Subramanyam, Y.V.B.K.; Shanthi, G.; Jagannatha, R.
 Gene 81, 219-226, 1989
 A;Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escherichia coli
 A;Reference number: A33068; MUID:90034194; PMID:2680769
 A;Accession: A33068
 A;Molecule type: DNA
 A;Residues: 1-18, A', 20-72 <DWA>
 A;Cross-references: GB:M29255; NID:g148029; PIDN:AAA24686.1; PID:g148030
 A;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
 R;Aimoto, S.; Takao, T.; Shimonishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T.
 Eur. J. Biochem. 129, 257-263, 1982
 A;Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic Escherichia coli
 A;Reference number: A33067; MUID:83105138; PMID:6759126
 A;Accession: A33067
 A;Molecule type: protein
 A;Residues: 54-72 <AIN>
 R;Guzman-Verduzco, L.M.; Kupersztosch, Y.M.
 Infect. Immun. 57, 645-648, 1989
 A;Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences
 A;Reference number: A30567; MUID:89108616; PMID:2643580
 A;Accession: A30567
 A;Molecule type: DNA

A:Residues: 1-18,'A',20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
A:Cross-references: GB:M18345; NID:g145862; PIDN:AAA23729.1; PID:g145863
C:Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.

C:Genetics: et
A:Gene: et
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
C:Keywords: enterotoxin; heat-stable protein
F:1-53/Domain: signal sequence and propeptide #status predicted <SIG>
F:54-72/Product: heat-stable enterotoxin ST-Ib #status experimental <MAT>
F:59-64,60-68,63-71/Disulfide bonds: #status experimental

Query Match 82.7%; Score 105; DB 1; Length 72;
Best Local Similarity 78.9%; Pred. No. 1.6e-05;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGCY 19
Db 54 NSSNYCCCLCCNPACTGCY 72

RESULT 6

S31652
enterotoxin - Yersinia kristensenii
C:Species: Yersinia kristensenii
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S31652
R:Ibrahim, A.; Liesack, W.; Stackebrandt, E.
submitted to the EMBL Data Library, November 1992
A:Reference number: S31652
A:Accession: S31652

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-66 <IBR>
A:Cross-references: UNIPROT:P31518; EMBL:X69218; NID:g48617; PIDN:CAA49152.1; PID:g48618
C:Superfamily: heat-stable enterotoxin ST

Query Match 70.1%; Score 89; DB 2; Length 66;
Best Local Similarity 85.7%; Pred. No. 0.00097;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YCCCLCCNPACAGC 18
Db 53 WCCVCCNPACAGC 66

RESULT 7

S68705
heat-stable enterotoxin Y-Stc - Yersinia enterocolitica
C:Species: Yersinia enterocolitica
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: S68705
R:Yoshino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y.
FEBS Lett. 362, 319-322, 1995
A:Title: Characterization of a highly toxic, large molecular size heat-stable enterotoxin
A:Reference number: S68705; MUID:95246844; PMID:7729521
A:Accession: S68705

A:Molecule type: protein
A:Residues: 1-53 <YOS>
A:Experimental source: strain 86-11
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:41-46,42-50,45-53/Disulfide bonds: #status predicted

Query Match 69.3%; Score 88; DB 2; Length 53;
Best Local Similarity 72.2%; Pred. No. 0.0011;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNTFYCCCLCCNPACAGC 18
Db 36 NDWDVCCCLCCNPACFGC 53

RESULT 8

S25659
heat-stable enterotoxin yst precursor - Yersinia enterocolitica
C:Species: Yersinia enterocolitica
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S25659; A41474; A23114; S65849
R:Ibrahim, A.; Liesack, W.; Pike, S.; Stackebrandt, E.
FEMS Microbiol. Lett. 97, 63-66, 1992
A:Title: The polymerase chain reaction: an epidemiological tool to differentiate between
A:Reference number: S25659
A:Accession: S25659

A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-71 <IBR>
A:Cross-references: UNIPROT:P07593; EMBL:X65999; NID:g48611; PIDN:CAA46801.1; PID:g48612
R:Delor, I.; Kaechenbeeck, A.; Wauters, G.; Cornelis, G.R.
Infect. Immun. 58, 2983-2988, 1990

A:Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-
A:Reference number: A41474; MUID:90354067; PMID:2201642
A:Accession: A41474

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: protein
A:Residues: 1-47,'S',49-71
A:Cross-references: GB:U09235; NID:g487394; PIDN:AAA18472.1; PID:g487395
R:Takao, T.; Tominaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A.
Eur. J. Biochem. 152, 199-206, 1985

A:Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced
A:Reference number: A23114; MUID:86004705; PMID:4043080
A:Accession: A23114

A:Molecule type: protein
A:Residues: 54-71 <TAK>
R:Mikulskis, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.
Mol. Microbiol. 14, 905-915, 1994
A:Title: Regulation of the Yersinia enterocolitica enterotoxin yst gene. Influence of gr
A:Reference number: S65849; MUID:952331297; PMID:7715452
A:Accession: S65849

A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-43 <MIK>
A:Cross-references: EMBL:U09235

C:Genetics: et
A:Gene: yst
C:Superfamily: heat-stable enterotoxin ST
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-41/Domain: propeptide #status predicted <PRO>
F:42-71/Product: heat-stable enterotoxin yst #status predicted <MAT>

Query Match 66.1%; Score 84; DB 2; Length 71;
Best Local Similarity 84.6%; Pred. No. 0.0037;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCELCNCPACAGC 18
Db 59 CCDVCCNPACAGC 71

RESULT 9

QHVCI
heat-stable enterotoxin ST precursor - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 17-Mar-1987 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41469; A01824; S34464; S34466; S34465; S34463
R:Ogawa, A.; Kato, J.I.; Watanabe, H.; Nair, B.G.; Takeda, T.
Infect. Immun. 58, 3325-3329, 1990
A:Title: Cloning and nucleotide sequence of a heat-stable enterotoxin gene from Vibrio
A:Reference number: A41469; MUID:90382953; PMID:2205577
A:Accession: A41469

A:Molecule type: DNA
A:Residues: 1-78 <OGA>
A:Cross-references: UNIPROT:P04429; GB:M85198; GB:M36061; NID:g155237; PIDN:AAA64889.1;
R:Takao, T.; Shimonishi, Y.; Kobayashi, M.; Nishimura, O.; Arita, M.; Takeda, T.; Honda,
FEBS Lett. 193, 250-254, 1985

A:Title: Amino acid sequence of heat-stable enterotoxin produced by Vibrio cholerae non-
A:Reference number: A01824; MUID:86056320; PMID:4065341

A;Accession: A01824
A;Molecule type: protein
A;Residues: 62-78 <TAK>
A;Experimental source: non-O-1 serovar
F;Yoshino, K.; Miyachi, M.; Takao, T.; Bag, P.K.; Xiaozhe, H.; Nair, G.B.; Takeda, T.; S
FEBS Lett. 326, 83-86, 1993
A;Title: Purification and sequence determination of heat-stable enterotoxin elaborated b
A;Reference number: S34463; MUID:933114823; PMID:8325391
A;Accession: S34464
A;Status: preliminary
A;Molecule type: protein
A;Residues: 61-78 <Y03>
A;Accession: S34466
A;Status: preliminary
A;Molecule type: protein
A;Residues: 51-78 <Y05>
A;Accession: S34465
A;Status: preliminary
A;Molecule type: protein
A;Residues: 60-78 <Y02>
A;Accession: S34463
A;Status: preliminary
A;Molecule type: protein
A;Residues: 62-78 <Y04>
A;Superfamily: heat-stable enterotoxin ST
C;Keywords: enterotoxin; heat-stable protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-61/Domain: Propeptide #status predicted <PRO>
F;62-78/Product: heat-stable enterotoxin ST #status experimental <MAT>
F;62-69,65-73,68-76/Disulfide bonds: #status predicted

Query Match 66.1%; Score 84; DB 1; Length 78;
Best Local Similarity 70.6%; Pred. No. 0.0039;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NTFYCELCNCPACG 18
DB 60 NLIDCCICCNPCFGC 76

RESULT 10
A54534
heat-stable enterotoxin - Vibrio mimicus (fragment)
C;Species: Vibrio mimicus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996
C;Accession: A54534
R;Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.
FEMS Microbiol. Lett. 79, 105-110, 1991
A;Title: Purification and characterization of a heat-stable enterotoxin of Vibrio mimicu
A;Reference number: A54534
A;Accession: A54534
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <ARI>
C;Superfamily: heat-stable enterotoxin ST

Query Match 64.6%; Score 82; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 0.0026;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCELCNCPACG 18
DB 3 CCEICCNPCFGC 15

RESULT 11
S34671
heat-stable enterotoxin - Vibrio cholerae (fragment)
C;Species: Vibrio cholerae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34671
R;Rossolini, G.M.; Lombardi, G.; Guglielmetti, P.
submitted to the EMBL Data Library, July 1993

A;Description: Detection of the Vibrio cholerae heat-stable enterotoxin gene by polymera
A;Reference number: S34671
A;Accession: S34671
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <ROS>
A;Cross-references: UNIPROT:Q56643; EMBL:X74108
C;Superfamily: heat-stable enterotoxin ST

Query Match 55.9%; Score 71; DB 2; Length 65;
Best Local Similarity 71.4%; Pred. No. 0.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NTFYCELCNCPAC 15
DB 51 NLIDCCICCNPCAC 64

RESULT 12
A45910
ultra-high-sulfur keratin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C;Accession: A45910
R;McNab, A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.
J. Invest. Dermatol. 92, 263-266, 1989
A;Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.
A;Reference number: A45910; MUID:89140394; PMID:2465353
A;Accession: A45910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <MCN>
A;Cross-references: UNIPROT:Q64526; GB:M27685; NID:G341749; PIDN:AAA81560.1; PID:G106681
C;Superfamily: ultra-high-sulfur keratin

Query Match 49.2%; Score 62.5; DB 2; Length 186;
Best Local Similarity 45.5%; Pred. No. 1.8;
Matches 10; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

QY 5 YCCELCNCPACAG-----CY 19
DB 140 FCLNLCQCPACSGPVTCTRTCY 161

RESULT 13
JC4651
uroguanylin precursor - human
N;Alternate names: guanylyl cyclase activating peptide II
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4651; S63702; S68052
R;Miyazato, M.; Nakazato, M.; Yamaguchi, H.; Date, Y.; Kojima, M.; Kangawa, K.; Matsuo, F.
Biochem. Biophys. Res. Commun. 219, 644-648, 1996
A;Title: Cloning and characterization of a cDNA encoding a precursor for human uroguanylin
A;Reference number: JC4651; MUID:96193705; PMID:8605041
A;Accession: JC4651
A;Molecule type: mRNA
A;Residues: 1-112 <MIY>
A;Cross-references: UNIPROT:Q16661; GB:U34279; NID:G1236798; PIDN:AAC50416.1; PID:G123679
R;Hill, O.; Cetin, Y.; Cieslak, A.; Maegert, H.J.; Forssmann, W.G.
Biochim. Biophys. Acta 1253, 146-149, 1995
A;Title: A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): precu
A;Reference number: S63702; MUID:96106424; PMID:8513795
A;Accession: S63702
A;Molecule type: mRNA
A;Residues: 1-112 <HIL>
A;Cross-references: EMBL:Z50753; NID:G974823; PIDN:CAA90629.1; PID:G974824
A;Experimental source: tissue colon
R;Hess, R.; Kuhn, M.; Schulz-Knappe, P.; Raida, M.; Fuchs, M.; Klodt, J.; Adermann, K.; I
FEBS Lett. 374, 34-38, 1995
A;Title: GCAP-II: isolation and characterization of the circulating form of human uroguar
A;Reference number: S68052; MUID:96049550; PMID:7589507
A;Accession: S68052

A:Molecule type: protein
 A:Residues: 89-99,'X',101-102,'X',104-107,'X',109-110,'X',112 <HES>
 C:Comment: This protein, a member of the guanylin peptide family, is an endogenous activ
 C:Superfamily: guanylin
 C:Keywords: intestine
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-112/Product: uroguanylin #status predicted <MAT>

Query Match 45.7%; Score 58; DB 2; Length 112;
 Best Local Similarity 75.0%; Pred. No. 4.2;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CELCNPACAGC 18
 |||||
 DB 100 CELCVNACTGC 111

RESULT 14

JC7620
 guanylin precursor, long form - European eel
 C:Species: Anguilla anguilla (European eel)
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C:Accession: JC7620
 R:Comrie, M.M.; Cutler, C.P.; Cramb, G.
 Biochem. Biophys. Res. Commun. 281, 1078-1085, 2001
 A:Title: Cloning and expression of guanylin from the European eel (Anguilla anguilla).
 A:Reference number: JC7620; MUID:21139737; PMID:11243845
 A:Accession: JC7620
 A:Molecule type: mRNA
 A:Residues: 1-116 <COM>
 A:Cross-references: GB:AJ301673
 C:Comment: This protein, a member of a family of heat-stable peptides, is a potent extra
 axis. This peptide signalling system plays a role in osmoregulation in euryhaline telec
 C:Superfamily: guanylin
 C:Keywords: heat-stable protein; osmoregulation
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-116/Product: guanylin precursor, long form #status predicted <MAT>
 F:33-39/Region: homologous #status predicted
 F:69-114/Region: highly conserved #status predicted

Query Match 45.7%; Score 58; DB 2; Length 116;
 Best Local Similarity 66.7%; Pred. No. 4.3;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 CELCNPACAGC 18
 |||||
 DB 104 CEICANAACTGC 115

RESULT 15

JC6548
 high sulfur protein b2F - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C:Accession: JC6548
 R:Mitsui, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Teuboi, R.; Ogawa, H.
 Gene 208, 123-129, 1998
 A:Title: Structure and hair follicle-specific expression of genes encoding the rat high
 A:Reference number: JC6547; MUID:98201605; PMID:9554245
 A:Accession: JC6548
 A:Molecule type: DNA
 A:Residues: 1-122 <MIT>
 A:Cross-references: UNIPROT:O70149; DBJ:AB003753; NID:G3046870; PIDN:BAA25574.1; PID:G3
 C:Comment: This protein is a cysteine-rich, keratin associated protein.
 C:Genetics:
 A:Gene: b2F
 C:Superfamily: keratin high-sulfur matrix protein IIIA

Query Match 44.5%; Score 56.5; DB 2; Length 122;
 Best Local Similarity 60.0%; Pred. No. 6.5;
 Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 5 YCELCNPPACAGCY 19
 |||||
 DB 107 YCGQCCRPACC-CY 120

Search completed: March 26, 2005, 16:49:39
 Job time : 5.0219 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:35:58 ; Search time 19.708 Seconds
(without alignments)
353.241 Million cell updates/sec

Title: US-10-775-481A-3
Perfect score: 121
Sequence: 1 NTFYCCBLCCYPACAGCN 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	100.0	18	1 AAP40186	Aap40186 Sequence
2	121	100.0	18	2 AAR85947	Aar85947 ST I* rec
3	121	100.0	18	2 AAY40509	Aay40509 ST recept
4	121	100.0	18	5 AAU93984	Aau93984 E. coli S
5	121	100.0	18	7 ADE10846	Adel10846 Chimeric
6	121	100.0	18	7 ADM39751	Adm39751 Escherich
7	121	100.0	18	8 ADG63946	Adg63946 Recombina
8	121	100.0	18	8 ADP73480	Adp73480 Escherich
9	121	100.0	18	8 ADR12773	Adr12773 E. coli S
10	121	100.0	18	8 ADR48343	Adr48343 Bacterial
11	121	100.0	18	8 ADR48331	Adr48331 E. coli S
12	121	100.0	18	8 ADR45823	Adr45823 Amino aci
13	121	100.0	36	1 AAP30263	Aap30263 Sequence
14	115	95.0	17	2 AAR85966	Aar85966 ST I* rec
15	115	95.0	17	2 AAR85961	Aar85961 ST I* rec
16	115	95.0	17	2 AAY40528	Aay40528 ST recept
17	115	95.0	17	2 AAY40523	Aay40523 ST recept
18	115	95.0	17	8 ADR45837	Adr45837 Amino aci
19	115	95.0	17	8 ADR45842	Adr45842 Amino aci
20	114	94.2	18	1 AAP40636	Aap40636 Sequence
21	110	90.9	16	2 AAR85967	Aar85967 ST I* rec
22	110	90.9	16	2 AAY40529	Aay40529 ST recept
23	110	90.9	16	8 ADR45843	Adr45843 Amino aci
24	109	90.1	16	2 AAR85962	Aar85962 ST I* rec
25	109	90.1	16	2 AAY40524	Aay40524 ST recept

26	109	90.1	16	8 ADR45838	Adr45838 Amino aci
27	107	88.4	46	1 AAP50436	Aap50436 Network p
28	106	87.6	17	2 AAR85951	Aar85951 ST Ia rec
29	106	87.6	17	2 AAY40546	Aay40546 ST recept
30	106	87.6	17	2 AAY40513	Aay40513 ST recept
31	106	87.6	17	8 ADR45827	Adr45827 Amino aci
32	106	87.6	17	8 ADR45860	Adr45860 Amino aci
33	106	87.6	18	2 AAR85956	Aar85956 ST Ia rec
34	106	87.6	18	2 AAR85981	Aar85981 ST I* rec
35	106	87.6	18	2 AAR85950	Aar85950 ST Ia rec
36	106	87.6	18	2 AAY40543	Aay40543 ST recept
37	106	87.6	18	2 AAY40518	Aay40518 ST recept
38	106	87.6	18	2 AAY40544	Aay40544 ST recept
39	106	87.6	18	2 AAY40512	Aay40512 ST recept
40	106	87.6	18	2 AAY02385	Aay02385 Heat stab
41	106	87.6	18	2 AAY29607	Aay29607 Escherich
42	106	87.6	18	2 AAY02397	Aay02397 Heat stab
43	106	87.6	18	8 ADR48330	Adr48330 E. coli S
44	106	87.6	18	8 ADR48332	Adr48332 C. freund
45	106	87.6	18	8 ADR48341	Adr48341 Bacterial

ALIGNMENTS

RESULT 1
AAP40186
ID AAP40186 standard; peptide; 18 AA.
XX AC AAP40186;
XX DT 25-MAR-2003 (revised)
DT 04-FEB-1992 (first entry)
XX XX
DE Sequence of monomeric synthetic heat-stable Escherichia coli enterotoxin
DE IB analogue VII.
XX KW Vaccine; diarrhoea; diagnosis; antigen.
XX OS Escherichia coli.
XX PN W08402700-A.
XX PD 19-JUL-1984.
XX PF 21-DEC-1983; 83WO-US002008.
XX PR 03-JAN-1983; 83US-00455265.
PR 12-DEC-1983; 83US-00559469.
PR 12-DEC-1984; 84WO-US002030.
(SCRI) SCRIPPS CLINIC & RES FOUND.
FI Houghten RA;
XX WPI; 1984-188753/30.
DR Synthetic polypeptide(s) with antigenicity of E.coli enterotoxin - useful
PT for vaccination against diarrhoea and for diagnostic tests.
XX Example; Page 53; 177pp; English.
CC The peptides of the invention can be used in a vaccine useful for
CC conferring protection against diarrhoea. They may also be used in a
CC diagnostic or reagent system for assaying for infections caused by the
CC E.coli strains. (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. NO. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 2
AAR85947
ID AAR85947 standard; peptide; 18 AA.
XX
AC AAR85947;
XX
DT 19-JAN-1996 (first entry)
XX
DE ST I* receptor ligand portion.
XX
KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
KW colorectal; metastasis.
XX
OS Escherichia coli.
XX
PN WO9511694-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012232.
XX
PR 26-OCT-1993; 93US-00141892.
PR 13-SEP-1994; 94US-00305056.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Waldman SA;
XX
DR WPI; 1995-178646/23.
XX
PT Conjugated cpds. which specifically bind to colorectal cancer cells -
PT comprise heat-stable toxin receptor binding moiety and active moiety
PT which may be a therapeutic agent or a radioactive agent.
XX
PS Claim 3; Page 116; 133pp; English.
XX
CC New conjugated compounds are provided which consist of (1) an ST receptor
CC binding moiety and (2) an active moiety which is a radio- stable agent.
CC 'ST' refers to a heat stable toxin produced by E.coli and other
CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
CC isotope) or nucleic acid; and the compound is used for the detection,
CC imaging or treatment of colorectal tumours, particularly metastasised
CC tumours. The present sequence is a specific example of an ST receptor
CC binding peptide which can be used in the conjugate
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 3
AAY40509
ID AAY40509 standard; peptide; 18 AA.
XX
AC AAY40509;
XX
DT 03-DEC-1999 (first entry)
XX
DE ST receptor peptide ST I*.
XX
KW Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.

Escherichia coli.
US962220-A.
05-OCT-1999.
06-JUN-1995; 95US-00467920.
26-OCT-1993; 93US-00141892.
(UYJE-) UNIV JEFFERSON THOMAS.
Waldman SA;
WPI; 1999-571264/48.
Conjugated compound comprising a receptor moiety and active moiety,
useful for the treatment/prevention of colorectal cancer.
Claim 1; Col 21-22; 23pp; English.
The invention relates to a conjugated compound that comprises a ST (heat-
stable toxin) receptor moiety selected from one of the sequences shown in
CC AAY40508-Y40559 and an active moiety (antisense molecule). The compound
CC is useful for the treatment of colorectal cancer. The use of the
CC conjugated compound is advantageous compared to antibodies since it binds
CC specifically to colorectal cells and has no toxic effect on normal cells.
CC The present sequence represents the amino acid sequence of a ST receptor
CC peptide ST I*.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 4
AAU93984
ID AAU93984 standard; peptide; 18 AA.
XX
AC AAU93984;
XX
DT 02-JUL-2002 (first entry)
XX
DE E. coli ST B cell epitope #2.
XX
KW Immunogenic; hepatitis B core; HBc;
KW vaccine; B cell epitope; T cell epitope; immunostimulant.
XX
OS Escherichia coli.
XX
PN WO200214478-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-US041759.
XX
PR 16-AUG-2000; 2000US-0225843P.
PR 22-AUG-2000; 2000US-0226867P.
PR 15-AUG-2001; 2001US-00930915.
XX
PA (APOV-) APOVIA INC.
XX
PI Birkett AJ;
XX
DR WPI; 2002-257601/30.
XX

```

PT Novel recombinant hepatitis B core protein, termed as chimeric
 PT hepatitis B core protein, displays immunogenic epitopes at N-terminus,
 PT HBC immunogenic loop with linker for conjugated epitope and C-terminus.
 XX
 PS Disclosure; Page 38; 289pp; English.

XX The invention relates to a recombinant hepatitis B core protein,
 CC i.e. a chimeric hepatitis B core (HBC) protein (I), displaying one or
 CC more immunogenic epitopes at the N-terminus, HBC immunogenic loop (L) or
 CC C-terminus, or having a heterologous linker for a conjugated epitope in
 CC (L), and containing a Cys residue at, or near, the C-terminus that
 CC confers enhanced stability to the particles. A vaccine comprising (I) is
 CC useful for inducing an immune response in an inoculated host animal, by
 CC inoculating a host animal with the vaccine, and maintaining that
 CC inoculated animal for a time period sufficient for that animal to develop
 CC an immune response. The immunogenic particles formed using (I) are
 CC substantially free of binding to nucleic acids, and are most stable than
 CC the particles formed from otherwise identical HBC chimera that lack the C-
 CC terminal residue or in which a C-terminal Cys is replaced by another
 CC residue. The chimera particles are most stable on storage in aqueous
 CC compositions that are particles of similar sequence that lack any C-
 CC terminal Cys residues. The chimera molecule exhibits the self-assembly not
 CC exhibiting the nucleic acid binding of those native particles, and
 CC typically prepared in higher yield than similar particles that are free
 CC of a C-terminal Cys. The particles are often far more immunogenic than
 CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of
 CC particles assembled from the chimera molecules are enhanced as compared to
 CC similar particles assembled from chimera molecules lacking at least one C-
 CC terminal Cys. AAU93802-AAU93997 represent immunogenic HBC particles amino
 CC acid sequences and related sequences of the invention

XX Sequence 18 AA;

Query Match 100.0%; Score 121; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NTFYCCCLCCYPACAGCN 18
 |||||
 Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 5

ADAE10846

ID ADE10846 standard; peptide; 18 AA.

XX ADE10846;

XX 29-JAN-2004 (first entry)

XX Chimeric hepatitis B virus related B-cell epitope seqid 80.

XX hepatotropic; virucide; antiinflammatory; chronic hepatitis; vaccine;
 KW recombinant hepatitis B core chimeric protein; HBC chimeric protein;
 KW hepatitis B infection; T-cell stimulator; B-cell epitope.

XX Escherichia coli.

XX US2003198645-A1.

XX 23-OCT-2003.

XX 21-FEB-2003; 2003US-00372076.

XX 21-FEB-2002; 2002US-00080299.

XX 21-FEB-2002; 2002US-00082014.

XX (PAGE/) PAGE M.

XX (FRIE/) FRIEDE M.

XX Page M, Friede M;

XX

DR WPI; 2003-852775/79.

XX Treating chronic hepatitis B infection by administering a T cell-
 PT stimulating vaccine containing immunogenic particles having recombinant
 PT carboxy-terminal truncated hepatitis B core (HBC) chimeric protein
 PT molecules.

XX Disclosure; SEQ ID NO 80; 111pp; English.

XX The invention describes a method of treating chronic hepatitis comprising
 CC administering to a patient a T cell-stimulating amount of a vaccine,
 CC comprising immunogenic particles dissolved or dispersed in a diluent,
 CC where the immunogenic particles consists of recombinant hepatitis B core
 CC (HBC) chimeric protein molecules, and maintaining the patient to induce T
 CC cells activated against HBC. The methods and compositions of the present
 CC invention are useful for treating chronic hepatitis B infection. This is
 CC the amino acid sequence of a chimeric hepatitis B virus related B-cell
 CC epitope useful for expression within the HBV chimera at the N-terminus,
 CC within the immunogenic loop and/or at the C-terminus.

XX Sequence 18 AA;

Query Match 100.0%; Score 121; DB 7; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NTFYCCCLCCYPACAGCN 18

|||||

Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 6

ADM39751

ID ADM39751 standard; peptide; 18 AA.

XX ADM39751;

XX 03-JUN-2004 (first entry)

XX Escherichia coli B-cell peptide epitope expressed by HBC chimera Seq 83.

XX immunogenic; avian hepatitis B virus; nucleocapsid;

XX self assembled particle; immunogen; inoculum; vaccine; immunostimulant;

XX antibacterial; virucidal; B-cell epitope.

XX Escherichia coli.

XX WO2003072722-A2.

XX 04-SEP-2003.

XX 21-FEB-2003; 2003WO-US005315.

XX 21-FEB-2002; 2002US-0359129P.

XX (APOV-) APOVIA INC.

XX Birkett AJ, Peck B;

XX WPI; 2003-679948/64.

XX New recombinant chimera avian hepatitis B core protein molecule, useful as
 PT an immunogen for inducing a B cell or T cell response to produce
 PT antibodies, or as a vaccine against pathogens.

XX Disclosure; SEQ ID NO 83; 278pp; English.

XX This invention relates to novel recombinant immunogenic chimeric avian
 CC hepatitis B core (AHBC) nucleocapsid proteins. Specifically, it refers to
 CC an AHBC protein that has been engineered to display an immunogenic B cell
 CC or T cell epitope, exhibit enhanced stability and an absence of nucleic
 CC acid binding as a self assembled particle. The present invention
 CC describes the chimeric AHBC protein as truncated at the C-terminus and

CC containing introduced cysteine residues that confers an enhanced
CC stability in aqueous solution, an increased yield and more immunogenicity
CC than similar conjugates that lack N- or C-terminal cysteines.
CC Furthermore, a reduction in the number of positively charged residues
CC (lysine and arginine) towards the C-terminus prepares self-assembled
CC particles that are substantially free of nucleic acid binding. As such,
CC these chimeric particles can be used as immunogens of an inoculum that
CC induce a B cell or T cell response in an animal to produce antibodies. It
CC can also be useful for developing a vaccine to protect against the
CC pathogen from which the heterologous epitope or the hapten is derived.
CC Accordingly, these compositions exhibit immunostimulant, antibacterial
CC and virucidal activities. This peptide sequence is an exemplary B-cell
CC epitope peptide immunogen useful for both linkage to the linker residue
CC after expression of a contemplated chimera and for expression within an
CC HBC chimera of the invention.

XX
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 121; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACACGN 18
Db |||||
1 NTFYCCCLCCYPACACGN 18

RESULT 7

ADG63946
ID ADG63946 standard; peptide; 18 AA.

XX AC ADG63946;

XX 11-MAR-2004 (first entry)

XX Recombinant chimera hepatitis B core protein immunogenic epitope #71.

XX Recombinant chimera hepatitis B core protein; HBC; immunogenic epitope;
XX HBC immunodominant loop; immune response.

XX Escherichia coli.

XX US2003185858-A1.

XX 02-OCT-2003.

XX 21-FEB-2002; 2002US-00082014.

XX 15-AUG-2001; 2001US-00930915.

XX (BIRK/) BIRKETT A J.

XX Birkett AJ;

XX WPI; 2004-031988/03.

XX Recombinant chimera hepatitis B core protein molecule useful for preparing
PT vaccine or inoculum includes peptide-bonded heterologous immunogenic
PT epitope at N-terminus in the hepatitis B core immunodominant loop or C-
PT terminus of the chimera.

XX Disclosure; SEQ ID NO 79; 110pp; English.

XX The invention relates to a recombinant chimera hepatitis B core (HBC)
CC protein molecule that includes a peptide-bonded heterologous immunogenic
CC epitope at the N-terminus in the HBC immunodominant loop or the C-
CC terminus of the chimera, or a heterologous linker residue for a conjugated
CC epitope present in the loop. The invention also relates to an immunogenic
CC particle comprising the recombinant hepatitis B core chimera protein
CC molecules, a vaccine comprising the immunogenic particles dissolved or
CC dispersed in a diluent, a nucleic acid that encodes a recombinant HBC
CC protein molecule or its variant, analogue, or complement and a method for
CC inducing an immune response in an inoculated host animal comprising

CC inoculating a host animal with a vaccine and maintaining the inoculated
CC animal for a period of time sufficient to enable development of an immune
CC response. The recombinant chimera hepatitis B core protein molecule is
CC used in an immunogenic particle for preparing a vaccine useful for
CC inducing an immune response in an inoculated host animal. This sequence
CC represents an HBC protein immunogenic B cell epitope of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 121; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACACGN 18
Db |||||
1 NTFYCCCLCCYPACACGN 18

RESULT 8

ADP73480

ID ADP73480 standard; peptide; 18 AA.

XX AC ADP73480;

XX 09-SEP-2004 (first entry)

XX Escherichia coli B cell epitope of gene ST, SEQ ID 93.

XX transgenic animal; Hepatitis B virus nucleocapsid core protein; HBC;
KW enhanced stability; hepatotropic; virucide; immunology;
KW protein engineering; immunogen; vaccine; Hepatitis B infection.

XX Escherichia coli.

XX WO2004053091-A2.

XX 24-JUN-2004.

XX 10-DEC-2003; 2003WO-US039164.

XX 10-DEC-2002; 2002US-0432123P.

XX (APOV-) APOVIA INC.

XX Lyons K, Birkett AJ, Haron JA;

XX WPI; 2004-468859/44.

XX New recombinant chimera hepatitis B core (HBC) protein molecules useful in
PT the fields of immunology and protein engineering, in particular as an
PT immunogen in a vaccine for Hepatitis B infections.

XX Disclosure; SEQ ID NO 93; 338pp; English.

XX The invention relates to a novel recombinant chimera hepatitis B virus
CC nucleocapsid (core) protein (HBC), up to 600 or 380 amino acid residues
CC in length. The chimera protein is engineered for both enhanced stability
CC of self-assembled particles and the substantial absence of nucleic acid
CC binding by the particles. The invention further comprises: a recombinant
CC HBC protein chimera molecule that has a length of 135-365 amino acid
CC residues and contains four peptide-linked amino acid residue sequence
CC domains from the N-terminus that are denominated domains I, II, III and
CC IV. The invention also provides nucleic acids, polypeptides, host cells,
CC vectors and transgenic animals used in the methods of the invention. The
CC chimeric compositions of the invention have hepatotropic and virucide
CC activities. The methods and compositions of the present invention are
CC useful in the fields of immunology and protein engineering, in particular
CC for using a chimera hepatitis B virus nucleocapsid protein as an
CC immunogen in a vaccine for Hepatitis B infections. This sequence
CC represents a Hepatitis B virus nucleocapsid (core) protein related
CC polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 121; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |
DB 1 NTFYCCCLCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |

RESULT 9
ADRI2773
ID ADRI2773 standard; peptide; 18 AA.
AC ADRI2773;
DT 04-NOV-2004 (first entry)
DE E. coli ST B cell epitope #2.
XX HBV; chronic hepatitis; Hbc; nucleocapsid core protein; vaccine;
KW immunogen; immunogenic epitope; T cell; B cell; CD8+ cell; CD4+ cell;
KW cytotoxic T lymphocyte; toll-like receptor 4; toll-like receptor 9;
KW TLR-4; TLR-9; epitope.
XX Escherichia coli.
OS US2004156863-A1.
XX 12-AUG-2004.
XX 01-OCT-2003; 2003US-00677074.
PF 21-FEB-2002; 2002US-00080299.
PR 21-FEB-2002; 2002US-00082014.
PR 21-FEB-2003; 2003US-00372076.
XX (PAGE//) PAGE M.
PA (FRIE//) FRIEDE M.
PA (SCHM//) SCHMIDT A E.
PA (STOB//) STOB D.
XX Page M, Friede M, Schmidt AE, Stober D;
XX WPI; 2004-603322/58.
XX Treating chronic hepatitis, by administering vaccine comprising
PT immunogenic particles having recombinant hepatitis B core chimeric
PT protein molecules, that stimulates T cell, to patient chronically
PT infected with hepatitis B virus.
XX Disclosure; SEQ ID NO 80; 117pp; English.

CC The invention relates to treating chronic hepatitis, by administering a
CC vaccine comprising immunogenic particles having recombinant hepatitis B
CC core (Hbc) chimeric protein molecules (where truncated Hbc molecules are
CC linked N-terminally or C-terminally to an immunogenic epitope), that
CC stimulate T cell production, to a patient chronically infected with
CC hepatitis B virus, and maintaining patient for time sufficient to induce
CC T cells activated against Hbc. The chimeric proteins are still capable
CC self-assembling into particles upon expression in a host cell and are
CC substantially free of binding to nucleic acids, and the particles display
CC enhanced stability. Also included is enhancing (M2) the production of one
CC or more of gamma-producing CD8+, CD4+ T cells and cytotoxic T lymphocytes
CC against hepatitis B virus, involving administering to a patient
CC chronically infected with hepatitis B virus, a T cell-stimulating amount
CC of a vaccine comprising immunogenic particles dissolved or dispersed in a
CC diluent containing one or both of an agonist of toll-like receptor 4 and
CC receptor 9 (TLR-4 and TLR-9), the immunogenic particles comprising Hbc
CC chimeric protein molecules and maintaining the patient for a sufficient
CC time to induce T cells activated against Hbc. The immunogenic epitopes
CC may be B cell or T cell epitopes. The chimeric vaccine is useful for
CC treating a patient chronically infected with hepatitis B virus. The

CC present sequence is a B cell epitope suitable for inclusion in the
CC chimeric protein of the invention.
XX Sequence 18 AA;
SQ

Query Match 100.0%; Score 121; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |
DB 1 NTFYCCCLCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |

RESULT 10
ADR48343
ID ADR48343 standard; peptide; 18 AA.
XX ADR48343;
XX 04-NOV-2004 (first entry)
DT Bacterial ST peptide #4.
DE Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
XX anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
KW neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic;
KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
KW antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
KW heartburn; dyspepsia; gastroparensis; Crohn's disease; ulcerative colitis;
KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
KW retinopathy; nephropathy; headache; anxiety; sleep disorder.
XX Escherichia coli.
OS WO2004069165-A2.
XX 19-AUG-2004.
XX 28-JAN-2004; 2004WO-US002390.
XX 28-JAN-2003; 2003US-0443098P.
PR 15-MAY-2003; 2003US-0471288P.
PR 12-NOV-2003; 2003US-0519460P.
XX (MICR-) MICROBIA INC.
XX Currie MG, Mahajan-Miklos S;
XX WPI; 2004-604332/58.
XX Novel purified peptide capable of activating the guanylate cyclase C
PT receptor, useful for treating obesity, congestive heart failure and
PT benign prostatic hyperplasia.
XX Disclosure; Page 29; 93pp; English.

CC The invention relates to a purified peptide (P1) capable of activating
CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
CC pharmaceutical composition comprising the peptide of the invention. The
CC composition of the invention is useful for treating a gastrointestinal
CC disorder in a patient, which involves administering P1, where the
CC gastrointestinal disorder is gastrointestinal motility disorder,
CC irritable bowel syndrome, chronic constipation, a functional
CC gastrointestinal disorder, gastroesophageal reflux disease, functional
CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel

CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The PI/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. PI is useful in treating slow digestion or slow
 CC stomach emptying. PI is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. PI is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. PI is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycemia, respiratory disorders
 CC including inhalation. PI is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. PI is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. PI is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumors, etc. PI can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasis or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

XX Sequence 18 AA;

Query Match 100.0%; Score 121; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCELCVCPACAGCN 18
 DB 1 NTFYCCELCVCPACAGCN 18

RESULT 11

ADRA48331
 ID ADR48331 standard; peptide; 18 AA.

XX AC ADR48331;

XX DT 04-NOV-2004 (first entry)

XX DE E. coli ST I* peptide.

XX KW Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
 KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; auditory; antiemetic; antidiabetic;
 KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
 KW antidiabetic; ophthalmological; tranquilizer; hypnotic; nootropic;
 KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.

OS Escherichia coli.

XX PN WO2004069165-A2.

XX PD 19-AUG-2004.

XX PF 28-JAN-2004; 2004WO-US002390.

XX PR 28-JAN-2003; 2003US-0443098P.

XX PR 15-MAY-2003; 2003US-0471288P.

XX PR 12-NOV-2003; 2003US-0519460P.

XX KW

(MICR-) MICROBIA INC.

XX Currie MG, Mahajan-Miklos S;

XX WPI; 2004-604332/58.

XX Novel purified peptide capable of activating the guanylate cyclase C
 PT receptor, useful for treating obesity, congestive heart failure and
 PT benign prostatic hyperplasia.

XX Disclosure; Page 28; 93pp; English.

XX The invention relates to a purified peptide (PI) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering PI, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The PI/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. PI is useful in treating slow digestion or slow
 CC stomach emptying. PI is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. PI is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. PI is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycemia, respiratory disorders
 CC including inhalation. PI is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. PI is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. PI is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumors, etc. PI can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasis or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

XX Sequence 18 AA;

Query Match 100.0%; Score 121; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCELCVCPACAGCN 18
 DB 1 NTFYCCELCVCPACAGCN 18

RESULT 12

ADRA45823

ID ADR45823 standard; peptide; 18 AA.

XX AC ADR45823;

XX DT 18-NOV-2004 (first entry)

XX DE Amino acid sequence of peptide ST I* inhibiting ST activity.

XX KW heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
 KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
 KW ST Ia.

XX OS Unidentified.
 XX PN WO2004071436-A2.
 XX PD 26-AUG-2004.
 XX PF 10-FEB-2004; 2004WO-US003765.
 XX PR 10-FEB-2003; 2003US-0446730P.
 XX PA (UWJE-) UNIV JEFFERSON THOMAS.
 XX PI Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;
 XX DR WPI; 2004-615913/59.
 XX XX Increasing ST receptor molecules on the surface of a colorectal, gastric
 PT or esophageal cancer cell to treat these cancers comprises administering
 PT ST receptor ligand molecules that bind to ST receptors on the surface of
 PT the cancer cell.
 XX PS Claim 6; SEQ ID NO 3; 97pp; English.
 XX CC The specification describes a method for increasing the number of heat
 CC stable toxin (ST) receptor molecules on the surface of a metastasised
 CC colorectal cancer cell. The method comprises administering, by continuous
 CC infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
 CC per hour for at least 6 hours, where ST receptor ligand molecules bind to
 CC ST receptors on the surface of the cancer cell in the individual and the
 CC number of ST receptor molecules on the surface of the cancer cell is
 CC increased. Therapeutic compositions comprising components which target ST
 CC receptors can then be used to inhibit proliferation of the colorectal,
 CC gastric and esophageal cells. This method may be used for treating
 CC individuals that have diseases that affect colorectal, gastric and
 CC esophageal cells, including colorectal, gastric or esophageal cancers.
 CC The present sequence represents a peptide which inhibits ST activity, and
 CC is designated ST I*. It is used as the ST receptor ligand in the method
 CC of the invention.
 XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 121; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NTFYCCCLCCYPACAGCN 18
 Db 1 NTFYCCCLCCYPACAGCN 18
 RESULT 13
 AAP30263
 ID AAP30263 standard; peptide; 36 AA.
 XX AC AAP30263;
 XX XX 25-MAR-2003 (revised)
 DT 25-APR-1992 (first entry)
 XX DE Sequence of peptide used to vaccinate against E. coli enterotoxin(s).
 XX KW Vaccine; enterotoxin; diarrhoea; immunogen.
 XX OS Escherichia coli.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1..18
 FT /label= Peptide P
 XX PN EP93652-A.
 XX PD 09-NOV-1983.

XX 26-APR-1983; 83EP-00400827.
 XX 26-APR-1982; 82EP-00007179.
 XX (INSP) INST PASTEUR.
 XX (CNRS) CENT NAT RECH SCI.
 XX Tartar A, Dufloot E, Boquet P;
 XX WPI; 1983-816301/46.
 XX Peptide(s) used to vaccinate against E. coli enterotoxin(s) - contg. e.g.
 PT asparagine threonine phenylalanine tyrosine cysteine glutamic
 PT acid leucine cysteine asparagine sequences.
 XX Claim 1; Page 40; 50pp; French.
 XX The inventors claim peptides of formula (P)n (see FT; see also AAP30263)
 CC having 4n-18n amino acids and pref. being laevorotatory (where n is 1 or
 CC 2). In AAP30262 and AAP30263, N=2. When n is 2, the peptide comprises two
 CC peptide sequences P, which may be the same or different, each having 4-18
 CC amino acids chosen from the peptide P SQ in AAP30262 or AAP30263. The two
 CC P sequences may be joined (a) by a disulphide bond or (b) by a bond
 CC formed between a carboxyl gp. of one sequence of an amino gp. of the
 CC other. (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 36 AA;
 Query Match 100.0%; Score 121; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 9.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NTFYCCCLCCYPACAGCN 18
 Db 1 NTFYCCCLCCYPACAGCN 18
 RESULT 14
 AAR85966
 ID AAR85966 standard; peptide; 17 AA.
 XX AC AAR85966;
 XX DT 19-JAN-1996 (first entry)
 XX DE ST I* receptor ligand portion.
 XX KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
 XX colorectal; metastasis.
 XX OS Escherichia coli.
 XX PN WO9511694-A1.
 XX PD 04-MAY-1995.
 XX PF 26-OCT-1994; 94WO-US012232.
 XX PR 26-OCT-1993; 93US-00141892.
 XX PR 13-SEP-1994; 94US-00305056.
 XX PA (UWJE-) UNIV JEFFERSON THOMAS.
 XX PI Waldman SA;
 XX DR WPI; 1995-178646/23.
 XX PT Conjugated cpds. which specifically bind to colorectal cancer cells -
 PT comprise heat-stable toxin receptor binding moiety and active moiety
 PT which may be a therapeutic agent or a radioactive agent.
 XX PS Claim 3; Page 120; 133pp; English.

XX New conjugated compounds are provided which consist of (1) an ST receptor
 CC binding moiety and (2) an active moiety which is a radio- stable agent.
 CC 'ST' refers to a heat stable toxin produced by E.coli and other
 CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
 CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
 CC isotope) or nucleic acid; and the compound is used for the detection,
 CC imaging or treatment of colorectal tumours, particularly metastasised
 CC tumours. The present sequence is a specific example of an ST receptor
 CC binding peptide which can be used in the conjugate
 XX

SQ Sequence 17 AA;

Query Match 95.0%; Score 115; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 2.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TFCYCELCYCPACAGC 18
 |||||
 Db 1 TFCYCELCYCPACAGC 17

RESULT 15
 AAR85961
 ID AAR85961 standard; peptide; 17 AA.

XX AC AAR85961;

XX DT 19-JAN-1996 (first entry)

XX DE ST I* receptor ligand portion.

XX KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
 XX colorectal; metastasis.

XX OS Escherichia coli.

XX FN WO9511694-A1.

XX PD 04-MAY-1995.

XX PF 26-OCT-1994; 94WO-US012232.

XX PR 26-OCT-1993; 93US-00141892.

XX PR 13-SEP-1994; 94US-00305056.

XX PA (UJVE-) UNIV JEFFERSON THOMAS.

XX PI Waldman SA;

XX DR WPI; 1995-178646/23.

XX PT Conjugated cpds. which specifically bind to colorectal cancer cells -
 PT comprise heat-stable toxin receptor binding moiety and active moiety
 PT which may be a therapeutic agent or a radioactive agent.

XX PS Claim 3; Page 119; 133pp; English.

XX New conjugated compounds are provided which consist of (1) an ST receptor
 CC binding moiety and (2) an active moiety which is a radio- stable agent.
 CC 'ST' refers to a heat stable toxin produced by E.coli and other
 CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
 CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
 CC isotope) or nucleic acid; and the compound is used for the detection,
 CC imaging or treatment of colorectal tumours, particularly metastasised
 CC tumours. The present sequence is a specific example of an ST receptor
 CC binding peptide which can be used in the conjugate
 XX

SQ Sequence 17 AA;

Query Match 95.0%; Score 115; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 2.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NTFYCCELCCYPACAGC 17
 |||||
 Db 1 NTFYCCELCCYPACAGC 17

Search completed: March 26, 2005, 16:44:27
 Job time : 20.708 secs

RESULT 2
US-08-583-447A-3
; Sequence 3, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583.447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-583-447A-3
Query Match 100.0%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NTFYCCELCCYPACAGCN 18
Db 1 NTFYCCELCCYPACAGCN 18
RESULT 3
US-08-467-920-3
; Sequence 3, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-467-920-3
Query Match 100.0%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NTFYCCELCCYPACAGCN 18
Db 1 NTFYCCELCCYPACAGCN 18
RESULT 4
US-08-635-930-3
; Sequence 3, Application US/08635930
; Patent No. 6060037
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-635-930-3

Query Match 100.0%; Score 121; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACGCN 18
Db 1 NTFYCCCLCCYPACGCN 18

RESULT 5
US-09-193-997-3
Sequence 3, Application US/09193997

PATENT No. 6087109
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-193-997-3

Query Match 100.0%; Score 121; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACGCN 18

Db 1 NTFYCCCLCCYPACGCN 18

RESULT 6

US-09-138-237A-3
Sequence 3, Application US/09138237A

PATENT No. 6268159
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,237A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/141,892

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-0903

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-138-237A-3

Query Match 100.0%; Score 121; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACGCN 18

Db 1 NTFYCCCLCCYPACGCN 18

RESULT 7

US-08-141-892A-18

Sequence 18, Application US/08141892A
PATENT No. 5518888

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and Methods

TITLE OF INVENTION: Of Using the Same

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5 inch disk, 720 Kb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/141.892A
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-0903
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-141-892A-18
;;
Query Match 95.0%; Score 115; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NTFYCCELCCYPACAGC 17
Db 1 NTFYCCELCCYPACAGC 17
;;
RESULT 8
US-08-141-892A-23
; Sequence 23, Application US/08141892A
; Patent No. 551888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-141-892A-23
;;
Query Match 95.0%; Score 115; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TFYCCELCCYPACAGCN 18
Db 1 TFYCCELCCYPACAGCN 17
;;
RESULT 9
US-08-583-447A-18
; Sequence 18, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-583-447A-18
;;
Query Match 95.0%; Score 115; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NTFYCCELCCYPACAGC 17
Db 1 NTFYCCELCCYPACAGC 17
;;
RESULT 10
US-08-583-447A-23
; Sequence 23, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.

;; TITLE OF INVENTION: ST Receptor Binding Compounds and
;; TITLE OF INVENTION: Methods of Using the Same
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656r1s
;; STREET: One Liberty Place, 46th Floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: WordPerfect 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/583,447A
;; FILING DATE: 05-JAN-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/141,892
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1702
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-583-447A-23
Query Match 95.0%; Score 115; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TFYCCELCCYPACACGN 18
Db 1 TFYCCELCCYPACACGN 17
RESULT 11
US-08-467-920-18
; Sequence 18, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5962220r1s
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/141,892
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1589
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-467-920-18
Query Match 95.0%; Score 115; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NTFYCCELCCYPACAGC 17
Db 1 NTFYCCELCCYPACAGC 17
RESULT 12
US-08-467-920-23
; Sequence 23, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5962220r1s
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-467-920-23

Query Match 95.0%; Score 115; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFYCCCLCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |
Db 1 TFYCCCLCCYPACAGCN 17

RESULT 13

US-08-635-930-18
; Sequence 18, Application US/08635930
; Patent No. 6060037

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: Compositions That Specifically Bind To

; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using

; TITLE OF INVENTION: The Same

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: WINDOWS 3.1

; SOFTWARE: WordPerfect 6.0/6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,930

; FILING DATE: 26-APR-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/141,892

; FILING DATE: 26-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/305,056

; FILING DATE: 13-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-1360

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-635-930-18

Query Match 95.0%; Score 115; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGC 17
| | | | | | | | | | | | | | | | | |
Db 1 NTFYCCCLCCYPACAGC 17

RESULT 14

US-08-635-930-23

; Sequence 23, Application US/08635930

; Patent No. 6060037

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: Compositions That Specifically Bind To

; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using

; TITLE OF INVENTION: The Same

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: WINDOWS 3.1

; SOFTWARE: WordPerfect 6.0/6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,930

; FILING DATE: 26-APR-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/141,892

; FILING DATE: 26-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/305,056

; FILING DATE: 13-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-1360

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-635-930-23

Query Match 95.0%; Score 115; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFYCCCLCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |
Db 1 TFYCCCLCCYPACAGCN 17

RESULT 15

US-09-193-997-18

; Sequence 18, Application US/09193997

; Patent No. 6087109

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: Compositions That Specifically

; TITLE OF INVENTION: Bind To Colorectal Cancer Cells

; TITLE OF INVENTION: And Methods Of Using The Same

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESSEE: No. 6087109ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-193-997-18

Query Match 95.0%; Score 115; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NTFYCCELCCYPACAGC 17
| | | | | | | | | | | | | | | | | |
Db 1 NTFYCCELCCYPACAGC 17

Search completed: March 26, 2005, 16:51:12
Job time : 6.38686 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:48:40 ; Search time 17.9343 Seconds
(without alignments)
332.314 Million cell updates/sec

Title: US-10-775-481A-3

Perfect score: 121

Sequence: 1 NTFYCCCLCCYPACAGCN 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	18	10	US-09-930-915A-289
2	121	100.0	18	14	US-10-082-014-79
3	121	100.0	18	14	US-10-372-076-80
4	121	100.0	18	15	US-10-621-684-3
5	121	100.0	18	16	US-10-806-006-289
6	121	100.0	18	16	US-10-677-074-80
7	121	100.0	18	16	US-10-805-913-289
8	121	100.0	18	17	US-10-796-719-3
9	115	95.0	17	15	US-10-621-684-18
10	115	95.0	17	15	US-10-621-684-23
11	110	90.9	16	15	US-10-621-684-24
12	109	90.1	16	15	US-10-621-684-19
13	106	87.6	17	15	US-10-621-684-8

14	106	87.6	17	15	US-10-621-684-41	Sequence 41, Appl
15	106	87.6	18	15	US-10-621-684-7	Sequence 7, Appl
16	106	87.6	18	15	US-10-621-684-13	Sequence 13, Appl
17	106	87.6	18	15	US-10-621-684-38	Sequence 38, Appl
18	106	87.6	18	15	US-10-621-684-39	Sequence 39, Appl
19	106	87.6	18	17	US-10-796-719-2	Sequence 2, Appl
20	106	87.6	18	17	US-10-796-719-4	Sequence 4, Appl
21	106	87.6	19	15	US-10-621-684-2	Sequence 2, Appl
22	106	87.6	72	17	US-10-796-719-20	Sequence 20, Appl
23	104	86.0	15	15	US-10-621-684-20	Sequence 20, Appl
24	104	86.0	15	15	US-10-621-684-25	Sequence 25, Appl
25	104	86.0	18	10	US-09-930-915A-290	Sequence 290, App
26	104	86.0	18	14	US-10-082-014-80	Sequence 80, Appl
27	104	86.0	18	14	US-10-372-076-81	Sequence 81, Appl
28	104	86.0	18	16	US-10-806-006-290	Sequence 290, App
29	104	86.0	18	16	US-10-677-074-81	Sequence 81, Appl
30	104	86.0	18	16	US-10-805-913-290	Sequence 290, App
31	100	82.6	16	15	US-10-621-684-9	Sequence 9, Appl
32	100	82.6	17	15	US-10-621-684-14	Sequence 14, Appl
33	98	81.0	14	15	US-10-621-684-21	Sequence 21, Appl
34	98	81.0	18	15	US-10-621-684-40	Sequence 40, Appl
35	98	81.0	18	17	US-10-796-719-11	Sequence 11, Appl
36	97	80.2	14	10	US-09-930-915A-288	Sequence 288, App
37	97	80.2	14	14	US-10-082-014-78	Sequence 78, Appl
38	97	80.2	14	14	US-10-372-076-79	Sequence 79, Appl
39	97	80.2	14	15	US-10-621-684-26	Sequence 26, Appl
40	97	80.2	14	16	US-10-806-006-288	Sequence 288, App
41	97	80.2	14	16	US-10-677-074-79	Sequence 79, Appl
42	97	80.2	14	16	US-10-805-913-288	Sequence 288, App
43	95	78.5	15	15	US-10-621-684-10	Sequence 10, Appl
44	95	78.5	16	15	US-10-621-684-15	Sequence 15, Appl
45	94	77.7	19	15	US-10-621-684-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-09-930-915A-289
; Sequence 289, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 289
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-930-915A-289

Query Match 100.0%; Score 121; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 2
US-10-082-014-79
; Sequence 79, Application US/10082014
; Publication No. US20030185858A1

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; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
; FILE REFERENCE: ICC-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/930,915
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-082-014-79

Query Match      100.0%; Score 121; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NTFYCCCLCCYPACAGCN 18
Db      1 NTFYCCCLCCYPACAGCN 18
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RESULT 3
US-10-372-076-80
; Sequence 80, Application US/10372076
; Publication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; TITLE OF INVENTION: CHRONIC HEPATITIS
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-372-076-80

Query Match      100.0%; Score 121; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NTFYCCCLCCYPACAGCN 18
Db      1 NTFYCCCLCCYPACAGCN 18
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RESULT 4
US-10-621-684-3
; Sequence 3, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA

Query Match      100.0%; Score 121; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NTFYCCCLCCYPACAGCN 18
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; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-621-684-3

Query Match      100.0%; Score 121; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NTFYCCCLCCYPACAGCN 18
Db      1 NTFYCCCLCCYPACAGCN 18
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RESULT 5
US-10-806-006-289
; Sequence 289, Application US/10806006
; Publication No. US20040152876A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/91644 ICC-102.2 DV I
; CURRENT APPLICATION NUMBER: US/10/806,006
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/41759
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 289
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-806-006-289

Query Match      100.0%; Score 121; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NTFYCCCLCCYPACAGCN 18
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Db 1 NTFYCCCLCCYPACGCN 18

RESULT 6

US-10-677-074-80

; Sequence 80, Application US/10677074

; Publication No. US20040156863A1

; GENERAL INFORMATION:

; APPLICANT: Page, Mark

; APPLICANT: Friede, Martin

; APPLICANT: Schmidt, Annette Elisabeth

; APPLICANT: Stober, Detlef

; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR

; TITLE OF INVENTION: CHRONIC HEPATITIS

; FILE REFERENCE: 4564/87179

; CURRENT APPLICATION NUMBER: US/10/677,074

; CURRENT FILING DATE: 2003-10-01

; PRIOR APPLICATION NUMBER: 10/372,076

; PRIOR FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: 10/080,299

; PRIOR FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: 10/082,014

; PRIOR FILING DATE: 2002-02-22

; NUMBER OF SEQ ID NOS: 308

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 80

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Escherichia coli

US-10-677-074-80

Query Match 100.0%; Score 121; DB 16; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.1e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACGCN 18

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Db 1 NTFYCCCLCCYPACGCN 18

RESULT 7

US-10-805-913-289

; Sequence 289, Application US/10805913

; Publication No. US20040156864A1

; GENERAL INFORMATION:

; APPLICANT: Birkett, Ashley J.

; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED

; TITLE OF INVENTION: STABILITY

; FILE REFERENCE: 4564/91645 ICC-102.2 DV II

; CURRENT APPLICATION NUMBER: US/10/805,913

; CURRENT FILING DATE: 2004-03-22

; PRIOR APPLICATION NUMBER: 09/930,915

; PRIOR FILING DATE: 2001-08-15

; PRIOR APPLICATION NUMBER: PCT/US01/41759

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/226,867

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: 60/225,843

; PRIOR FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 313

; SOFTWARE: Patent in ver. 2.1

; SEQ ID NO 289

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Escherichia coli

US-10-805-913-289

Query Match 100.0%; Score 121; DB 16; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.1e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACGCN 18

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Db 1 NTFYCCCLCCYPACGCN 18

RESULT 8

US-10-796-719-3

; Sequence 3, Application US/10796719

; Publication No. US20050020811A1

; GENERAL INFORMATION:

; APPLICANT: Currie, Mark G.

; APPLICANT: Mahajan-Miklos, Shalina

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS

; FILE REFERENCE: 14184-043001

; CURRENT APPLICATION NUMBER: US/10/796,719

; CURRENT FILING DATE: 2004-03-09

; PRIOR APPLICATION NUMBER: US 10/766,735

; PRIOR FILING DATE: 2004-01-28

; PRIOR APPLICATION NUMBER: US 60/443,098

; PRIOR FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: US 60/471,288

; PRIOR FILING DATE: 2003-05-15

; PRIOR APPLICATION NUMBER: US 60/519,460

; PRIOR FILING DATE: 2003-11-12

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Escherichia coli

US-10-796-719-3

Query Match 100.0%; Score 121; DB 17; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.1e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACGCN 18

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Db 1 NTFYCCCLCCYPACGCN 18

RESULT 9

US-10-621-684-18

; Sequence 18, Application US/10621684

; Publication No. US20040029182A1

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; TITLE OF INVENTION: ST Receptor Binding Compounds and

; TITLE OF INVENTION: Methods of Using the Same

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: Wordperfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/621,684

; FILING DATE: 17-Jul-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,447A

; FILING DATE: 05-JAN-1996

; APPLICATION NUMBER: US 08/141,892

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-621-684-18

Query Match 95.0%; Score 115; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGC 17
Db 1 NTFYCCCLCCYPACAGC 17

RESULT 10
US-10-621-684-23
Sequence 23, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-621-684-24

Query Match 90.9%; Score 110; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FYCCCLCCYPACAGCN 18
Db 1 FYCCCLCCYPACAGCN 16

RESULT 12
US-10-621-684-19
Sequence 19, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania

Qy 2 NTFYCCCLCCYPACAGCN 18

; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-621-684-19
Query Match 90.1%; Score 109; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TFCYCELCYPCACG 17
Db 1 TFCYCELCYPCACG 16
RESULT 13
US-10-621-684-8
; Sequence 8, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark

; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-621-684-8
Query Match 87.6%; Score 106; DB 15; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NTFYCCELCYPCACG 17
Db 1 NTFYCCELCYPCACG 17
RESULT 14
US-10-621-684-41
; Sequence 41, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-621-684-41
Query Match 87.6%; Score 106; DB 15; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGC 17
|||||
Db 1 NTFYCCCLCCNPACAGC 17
|||||

RESULT 15
US-10-621-684-7
; Sequence 7, Application US/10621684
; Publication No. US20040029182A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/621,684
; FILING DATE: 17-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-621-684-7

Query Match 87.6%; Score 106; DB 15; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGC 17
|||||
Db 2 NTFYCCCLCCNPACAGC 18
|||||

Search completed: March 26, 2005, 17:16:37
Job time : 17.9343 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:49 ; Search time 3.81022 Seconds
(without alignments)
454.541 Million cell updates/sec

Title: US-10-775-481A-3
Perfect score: 121
Sequence: 1 NTFYCCBLCVCPACAGCN 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	18	1 QHEC2	heat-stable entero
2	106	87.6	18	2 A60103	heat-stable entero
3	106	87.6	72	1 QHEC1	heat-stable entero
4	85	70.2	72	1 QHEC4	heat-stable entero
5	85	70.2	72	1 QHEC1B	heat-stable entero
6	81	66.9	66	2 S31652	enterotoxin - Yers
7	78	64.5	53	2 S68705	heat-stable entero
8	76	62.8	71	2 S25659	heat-stable entero
9	76	62.8	78	1 QHVC1	heat-stable entero
10	74	61.2	17	2 A54534	heat-stable entero
11	63	52.1	65	2 S34671	heat-stable entero
12	59	48.8	115	1 A46279	guanylin precursor
13	59	48.8	115	1 JN0318	guanylin precursor
14	59	48.8	116	1 B46279	guanylin precursor
15	59	48.8	186	2 A45910	ultra-high-sulfur
16	56	46.3	268	2 T20758	hypothetical prote
17	53.5	44.2	152	2 T18975	hypothetical prote
18	53.5	44.2	164	2 T24272	hypothetical prote
19	53.5	44.2	188	2 T15651	hypothetical prote
20	51	42.1	56	1 WTFP	testis-specific pr
21	51	42.1	68	2 S25775	testis-specific pr
22	51	42.1	141	2 H81810	hypothetical prote
23	51	42.1	525	2 G71317	hypothetical prote
24	51	42.1	589	2 T01709	hypothetical prote
25	51	42.1	652	2 T85017	probable CHP-rich
26	51	42.1	1065	2 T52054	cellulose synthase
27	50	41.3	55	2 S25774	testis-specific pr
28	50	41.3	112	2 JC4651	uroguanylin precu
29	50	41.3	116	2 JC7620	guanylin precursor

30	49.5	40.9	61	2 A37425	metallothionein 2
31	49.5	40.9	62	2 S54336	metallothionein-2a
32	49.5	40.9	62	2 S54335	metallothionein-2c
33	49	40.5	122	2 S13900	phospholipase A2 (
34	49	40.5	122	2 JG6548	high sulfur protei
35	49	40.5	138	2 E48188	phospholipase A2 (
36	49	40.5	152	1 KRSHHC	keratin high-sulfu
37	49	40.5	152	2 I47111	high-sulfur wool m
38	49	40.5	152	2 I47108	high-sulfur wool m
39	49	40.5	152	2 I47109	high-sulfur wool m
40	49	40.5	152	2 I47112	high-sulfur wool m
41	49	40.5	156	1 KRSHHB	keratin high-sulfu
42	49	40.5	162	2 I47107	high-sulfur wool m
43	49	40.5	172	1 KRSHHA	keratin high-sulfu
44	49	40.5	172	2 I47106	high-sulfur wool m
45	49	40.5	182	1 KRSHHD	keratin high-sulfu

ALIGNMENTS

RESULT 1

QHEC2

heat-stable enterotoxin ST-2 - Escherichia coli

C:Species: Escherichia coli

C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004

C:Accession: A01823

R:Chan, S.K.; Giannella, R.A.

J. Biol. Chem. 256, 7744-7746, 1981

A:Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat

A:Reference number: A01823; MUID:81264141; PMID:7021541

A:Accession: A01823

A:Molecule type: protein

A:Residues: 1-18 <CHA>

A:Cross-references: UNIPROT:P01560

A:Experimental source: strain 18D, serotype 0.42:k86:H37

C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced by

idues of the heat-stable enterotoxin ST-1.

C:Superfamily: heat-stable enterotoxin ST

C:Keywords: enterotoxin; heat-stable protein

F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>

F:5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 100.0%; Score 121; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NTFYCCBLCVCPACAGCN 18

|||||

Db 1 NTFYCCBLCVCPACAGCN 18

|||||

RESULT 2

A60103

heat-stable enterotoxin ST-1a - Citrobacter freundii

C:Species: Citrobacter freundii

C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

C:Accession: A60103

R:Guarino, A.; Giannella, R.; Thompson, M.R.

Infect. Immun. 57, 649-652, 1989

A:Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identifia

A:Reference number: A60103; MUID:89108617; PMID:2912902

A:Accession: A60103

A:Molecule type: protein

A:Residues: 1-18 <GUA>

A:Cross-references: UNIPROT:Q7M0U3

C:Superfamily: heat-stable enterotoxin ST

Query Match 87.6%; Score 106; DB 2; Length 18;

Best Local Similarity 94.1%; Pred. No. 5.6e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NTFYCCBLCVCPACAGC 17

Db 1 NTFYCCCLCCNPACAGC 17
|||||

RESULT 3

QHEC1
heat-stable enterotoxin ST-I precursor - Escherichia coli
N:Alternate names: heat-stable enterotoxin estal
C:Species: Escherichia coli
C:Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 09-Jul-2004
C:Accession: A01822; A30985; A36732; J03374; I51932
R:SO, M.; McCarthy, B.J.
Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980
A:Title: Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stable (S)
A:Reference number: A01822; MUID:81054703; PMID:6254008
A:Accession: A01822
A:Molecule type: DNA
A:Residues: 1-72 <LAZ>
R:Lazure, C.; Seidah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S.
Can. J. Biochem. Cell Biol. 61, 287-292, 1983
A:Title: Primary structure determination of Escherichia coli heat-stable enterotoxin of
A:Reference number: A30985; MUID:83284515; PMID:6349752
A:Accession: A30985
A:Molecule type: protein
A:Residues: 55-72 <LAZ2>
A:Experimental source: strain F11
R:Dallas, W.S.
J. Bacteriol. 172, 5490-5493, 1990
A:Title: The heat-stable toxin I gene from Escherichia coli 18D.
A:Reference number: A36732; MUID:90368614; PMID:2203756
A:Accession: A36732
A:Molecule type: DNA
A:Residues: 1-72 <DAL>
A:Cross-references: GB:M58746; NID:gl45860; PIDN:AAA62776.1; PID:gl45861
A:Experimental source: strain 18D
R:Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;
Plasmid 20, 42-53, 1988
A:Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri
A:Reference number: J03073; MUID:89202548; PMID:3071819
A:Accession: J03074
A:Molecule type: DNA
A:Residues: 1-72 <STI>
R:Seikizaki, T.; Akashi, H.; Terakado, N.
Am. J. Vet. Res. 46, 909-912, 1985
A:Title: Nucleotide sequences of the genes for Escherichia coli heat-stable enterotoxin
A:Reference number: I51932; MUID:85249571; PMID:2590268
A:Accession: I51932
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-69, 'p', 71-72 <RES>
A:Cross-references: GB:M25607; NID:gl47877; PIDN:AAA24653.1; PID:gl47878
C:Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic stra
tular sizes.
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-54/Domain: propeptide #status predicted <PRO>
F:55-72/Product: heat-stable enterotoxin ST-I #status experimental <MAT>
F:59-64, 60-68, 63-71/Disulfide bonds: #status predicted

Query Match 87.6%; Score 106; DB 1; Length 72;
Best Local Similarity 94.1%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCNPACAGC 17
|||||

RESULT 4

QHEC4
heat-stable enterotoxin STA4 precursor - Escherichia coli

C:Species: Escherichia coli
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: J03073; A35978
R:Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;
Plasmid 20, 42-53, 1988
A:Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri
A:Reference number: J03073; MUID:89202548; PMID:3071819
A:Accession: J03073
A:Molecule type: DNA
A:Residues: 1-72 <STI>
A:Cross-references: UNIPROT:P07965; GB:J03311; NID:gl47875; PIDN:AAA24652.1; PID:gl47876
R:Zhou, X.; Shen, L.P.; Chi, C.W.
Toxicon 28, 453-456, 1990
A:Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stable
A:Reference number: A35978; MUID:90273381; PMID:2190361
A:Accession: A35978
A:Molecule type: DNA
A:Residues: 1-72 <ZHO>
C:Genetics:
A:Gene: estA4
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-53/Domain: propeptide #status predicted <PRO>
F:54-72/Product: heat-stable enterotoxin #status predicted <MAT>
F:59-64, 60-68, 63-71/Disulfide bonds: #status predicted

Query Match 70.2%; Score 85; DB 1; Length 72;
Best Local Similarity 85.7%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YCCELCCTCPACAGC 17
|||||

Db 58 YCCELCCTCPACTGC 71
|||||

RESULT 5

QHECIB
heat-stable enterotoxin ST-Ib precursor - Escherichia coli
N:Alternate names: heat-stable enterotoxin ST-A2
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
R:Moseley, S.L.; Hardy, J.W.; Hug, M.I.; Echeverria, P.; Falkow, S.
Infect. Immun. 59, 1167-1174, 1993
A:Title: Isolation and nucleotide determination of a gene encoding a heat-stable enteroto
A:Reference number: J50292; MUID:83184648; PMID:6341230
A:Accession: J50292
A:Molecule type: DNA
A:Residues: 1-72 <MOS>
A:Cross-references: UNIPROT:Q47185; UNIPROT:P07965; GB:M34916; NID:gl46407; PIDN:AAA23990
R:Barakanath, P.; Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha, I.
Gene 81, 219-226, 1989
A:Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escheri
A:Reference number: A33068; MUID:90034194; PMID:2680769
A:Accession: A33068
A:Molecule type: DNA
A:Residues: 1-18, 'A', 20-72 <DWA>
A:Cross-references: GB:M29255; NID:gl48029; PIDN:AAA24686.1; PID:gl48030
R:Aimoto, S.; Takao, T.; Shimomishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T.
Eur. J. Biochem. 129, 257-263, 1982
A:Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic
A:Reference number: A33067; MUID:83105138; PMID:6759126
A:Accession: A33067
A:Molecule type: protein
A:Residues: 54-72 <AIM>
R:Guzman-Verduzco, L.M.; Kupersztocz, Y.M.
Infect. Immun. 57, 645-648, 1989
A:Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences
A:Reference number: A30567; MUID:89108616; PMID:2643580
A:Accession: A30567
A:Molecule type: DNA

A;Residues: 1-18,'A',20-24,'AG',27-41,'V',43-44,'N',46,'E',48,'S',50-72 <GUZ>
 A;Cross-references: GB:M18345; NID:G145862; PIDN:AAA23729.1; PID:G145863
 C;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
 C;Genetics:

A;Gene: st
 C;Superfamily: heat-stable enterotoxin ST
 C;Keywords: enterotoxin; heat-stable protein
 F;1-53/Domain: signal sequence and propeptide #status predicted <SIG>
 F;54-72/Product: heat-stable enterotoxin ST-Ib #status experimental <MAT>
 F;59-64,60-68,63-71/Disulfide bonds: #status experimental

Query Match 70.2%; Score 85; DB 1; Length 72;
 Best Local Similarity 85.7%; Pred. No. 0.0029;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YCCELCCYPACAGC 17
 Db 58 YCCELCCNPACTGC 71

RESULT 6

S31652
 enterotoxin - Yersinia kristensenii
 C;Species: Yersinia kristensenii
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S31652
 R;Ibrahim, A.; Liesack, W.; Stackebrandt, E.
 submitted to the EMBL Data Library, November 1992
 A;Reference number: S31652
 A;Accession: S31652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-66 <IBR>

A;Cross-references: UNIPROT:P31518; EMBL:X69218; NID:G48617; PIDN:CAA49152.1; PID:G48618

C;Superfamily: heat-stable enterotoxin ST

Query Match 66.9%; Score 81; DB 2; Length 66;
 Best Local Similarity 78.6%; Pred. No. 0.0077;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCCELCCYPACAGC 17
 Db 53 WCCEVCCNPACAGC 66

RESULT 7

S68705
 heat-stable enterotoxin Y-STC - Yersinia enterocolitica
 C;Species: Yersinia enterocolitica
 C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
 C;Accession: S68705
 R;Yoshino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y.
 FEBS Lett. 362, 319-322, 1995

A;Title: Characterization of a highly toxic, large molecular size heat-stable enterotoxin
 A;Reference number: S68705; MUID:95246844; PMID:7729521
 A;Accession: S68705

A;Molecule type: protein

A;Residues: 1-53 <YOS>

A;Experimental source: strain 86-11

C;Superfamily: heat-stable enterotoxin ST

C;Keywords: enterotoxin; heat-stable protein

F;41-46,42-50,45-53/Disulfide bonds: #status predicted

Query Match 64.5%; Score 78; DB 2; Length 53;
 Best Local Similarity 78.6%; Pred. No. 0.015; Mismatches 2; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YCCELCCYPACAGC 17
 Db 40 WCCEVCCNPACAGC 53

RESULT 8

S25659

heat-stable enterotoxin yst precursor - Yersinia enterocolitica
 C;Species: Yersinia enterocolitica

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C;Accession: S25659; A41474; A23114; S65849

R;Ibrahim, A.; Liesack, W.; Pike, S.; Stackebrandt, E.

FEMS Microbiol. Lett. 97, 63-66, 1992

A;Title: The polymerase chain reaction: an epidemiological tool to differentiate between

A;Reference number: S25659

A;Accession: S25659

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-71 <IBR>

A;Cross-references: UNIPROT:P07593; EMBL:X65999; NID:G48611; PIDN:CAA46801.1; PID:G48612

R;Delor, I.; Kaeckenbeeck, A.; Wauters, G.; Cornelis, G.R.

Infect. Immun. 58, 2983-2988, 1990

A;Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-

A;Reference number: A41474; MUID:90354067; PMID:2201642

A;Accession: A41474

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-47,'S',49-71

A;Cross-references: GB:U09235; NID:G487394; PIDN:AAA18472.1; PID:G487395

R;Takao, T.; Tominaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A.

Eur. J. Biochem. 152, 199-206, 1985

A;Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced

A;Reference number: A23114; MUID:86004705; PMID:4043080

A;Accession: A23114

A;Molecule type: protein

A;Residues: 54-71 <YAK>

R;Mikulek, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.

Mol. Microbiol. 14, 905-915, 1994

A;Title: Regulation of the Yersinia enterocolitica enterotoxin yst gene. Influence of gr

A;Reference number: S65849; MUID:95231297; PMID:7715452

A;Accession: S65849

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-43 <MIK>

A;Cross-references: EMBL:U09235

C;Genetics:

A;Gene: yst

C;Superfamily: heat-stable enterotoxin ST

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-41/Domain: propeptide #status predicted <PRO>

F;42-71/Product: heat-stable enterotoxin yst #status predicted <MAT>

Query Match 62.8%; Score 76; DB 2; Length 71;
 Best Local Similarity 76.9%; Pred. No. 0.029;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCELCYCPACAGC 17
 Db 59 CCEVCCNPACAGC 71

RESULT 9

QHVCI

heat-stable enterotoxin ST precursor - Vibrio cholerae

C;Species: Vibrio cholerae

C;Date: 17-Mar-1997 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: A41469; A01824; S34464; S34465; S34463

R;Ogawa, A.; Kato, J.I.; Watanabe, H.; Nair, B.G.; Takeda, T.

Infect. Immun. 58, 3325-3329, 1990

A;Title: Cloning and nucleotide sequence of a heat-stable enterotoxin gene from Vibrio

A;Reference number: A41469; MUID:90382953; PMID:2205577

A;Accession: A41469

A;Molecule type: DNA

A;Residues: 1-78 <OGA>

A;Cross-references: UNIPROT:P04429; GB:M85198; GB:M36061; NID:G155237; PIDN:AAA64889.1;

R;Takao, T.; Shimonishi, Y.; Kobayashi, M.; Nishimura, O.; Arita, M.; Takeda, T.; Honda,

FEBS Lett. 193, 250-254, 1985

A;Title: Amino acid sequence of heat-stable enterotoxin produced by Vibrio cholerae non-

A;Reference number: A01824; MUID:86056320; PMID:4065341

Query Match	52.1%	Score 63;	DB 2;	Length 65;
Best Local Similarity	64.3%;	Pred. No. 0.8;		
Matches	9;	Conservative	1;	Mismatches
			4;	Indels
			0;	Gaps
			0;	

A;Residues: 1-115 <DE1>
A;Cross-references: UNIPROT:Q02747; GB:M95174; NID:g306823; PID:AAA58625.1; PID:G306824
A;Note: sequence extracted from NCBI backbone (NCBIN:115377, NCBIPI:115378)
R;Wiegand, R.C.; Kato, J.; Huang, M.D.; Fok, K.F.; Kachur, J.F.; Currie, M.G.

FEBS Lett. 311, 150-154, 1992
A; Title: Human guanylin: cDNA isolation, structure, and activity.
A; Reference number: S29228; MUID: 93011964; PMID: 1327879

A:Residues: 1-115 <GB>
A:Cross-references: GIB; NID:g183414; PION:AAA35915.1; PID:g183415
R:Kuhn, M.; Raida, M.; Adermann, K.; Schulz-Knappe, P.; Gerzer, R.; Heim, J.M.; Forseman
FEBS Lett. 318, 205-209, 1993
A:Title: The circulating bioactive form of human guanylin is a high molecular weight pept
A:Reference number: S29807; MUID:93178628; PMID:805028
A:Accession: S29807
A:Molecule type: protein
A:Residues: 22-68 <KOH>
A:Experimental source: plasma
A:Note: amino-terminal sequencing of mature form and molecular weight of mature form by m
C:Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl c
n of the same receptor.

A:Map position: lp35-lp34
C:Superfamily: guanylin
C:Keywords: hormone; intestine
F:1-21/Domain: signal sequence
F:22-115/Product: guanylin
#status predicted <SIG>
#status experimental <WAT>

```
F:22-115/Product: guanylin #status experimental <MAT>

Query Match          48.8%; Score 59; DB 1; Length 115;
Best Local Similarity 66.7%; Pred. No. 3.1;
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```

QY      6  CELCCYPACAGC  17
      |||: ||| |||
Db      104 CEICAYAACTGC  115

RESULT 13
JN0318
guanylin precursor - rat

```

UN0318
quanylin precursor - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1992 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JN0318; A43345; A38184; S25489
R;Wiegand, R.C.; Kato, J.; Currie, M.G.
Biochem. Biophys. Res. Commun. 185, 812-817, 1992
A;Title: Rat guanylin cDNA: characterization of the precursor of an endogenous activator
A;Reference number: JN0318; MUID:92328783; PMID:1378267
A;Accession: JN0318
A;Molecule type: mRNA
A;Residues: 1-115 <WIE>
A;Cross-references: UNIPROT:P28902; GB:M93005; NID:g204540; PIDN:AAA41300.1; PID:g204541
R;Schulz, S.; Christman, T.D.; Garbers, D.L.
J. Biol. Chem. 267, 16019-16021, 1992
A;Title: Cloning and expression of guanylin. Its existence in various mammalian tissues.
A;Reference number: A43345; MUID:92355545; PMID:1379587
A;Accession: A43345
A;Molecule type: mRNA
A;Residues: 1-115 <SCH>
A;Cross-references: GB:M95493; NID:g204542; PIDN:AAA41302.1; PID:g204543
A;Experimental source: intestine
A;Note: sequence extracted from NCBI backbone (NCBIN:110474, NCBIP:110476)
R;Currie, M.G.; Fok, K.F.; Kato, J.; Moore, R.J.; Hamra, F.K.; Duffin, K.L.; Smith, C.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 947-951, 1992
A;Title: Guanylin: an endogenous activator of intestinal guanylate cyclase.
A;Reference number: A38184; MUID:92141235; PMID:1346555
A;Accession: A38184
A;Molecule type: protein
A;Residues: 101-115 <CUR>
A;Experimental source: jejunum
A;Note: sequence extracted from NCBI backbone (NCBIP:79480)
A;Note: purification included boiling in acetic acid; peptide has activity but may represent
R;Maegert, H.J.; Khun, M.; Kruhofer, M.; Forssmann, W.G.
submitted to the EMBL Data Library, August 1992
A;Reference number: S25489
A;Accession: S25489
A;Molecule type: mRNA
A;Residues: 101-115 <MAE>
A;Cross-references: EMBL:X67669; NID:g56343; PIDN:CAA47901.1; PID:g56344
C;Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl
n of the same receptor.
C;Superfamily: guanylin
C;Keywords: hormone; intestine
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-115/Product: guanylin #status predicted <MAT>

Query Match 48.8%; Score 59; DB 1; Length 115;
Best Local Similarity 66.7%; Pred. No. 3.1; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 1

Qy 6 CELCCYPACAGC 17
Db 104 CEICAYAACTGC 115

RESULT 14
B46279
guanylin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: A55643; B46279
R;Sciaky, D.; Kosiba, J.L.; Cohen, M.B.
Genomics 24, 583-587, 1994
A;Title: Genomic sequence of the murine guanylin gene.
A;Reference number: A55643; MUID:95229161; PMID:7713512
A;Accession: A55643
A;Molecule type: DNA
A;Residues: 1-116 <SCI>
A;Cross-references: UNIPROT:P33680; GB:U60528; GB:U09741; NID:g1480667; PIDN:AA05758.1;
R;de Sauvage, F.J.; Keshav, S.; Kuang, W.J.; Gillett, N.; Henzel, W.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 89, 9089-9093, 1992
A;Title: Precursor structure, expression, and tissue distribution of human guanylin.
A;Reference number: A46279; MUID:93028409; PMID:11409606
A;Accession: B46279

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-116 <DBI>
A;Cross-references: GB:M95175; NID:g309282; PIDN:AAA37758.1; PID:g309283
A;Note: sequence extracted from NCBI backbone (NCBIP:115379)
C;Comment: Guanylin is an endogenous ligand for an intestine-specific receptor guanylyl
n of the same receptor.
C;Genetics:
C;Introns: 25/3; 96/1
C;Superfamily: guanylin
C;Keywords: hormone; intestine
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-116/Product: guanylin #status predicted <MAT>

Query Match 48.8%; Score 59; DB 1; Length 116;
Best Local Similarity 66.7%; Pred. No. 3.2; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 1

Qy 6 CELCCYPACAGC 17
Db 105 CEICAYAACTGC 116

RESULT 15

A45910
ultra-high-sulfur keratin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C;Accession: A45910
R;McNab, A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.
J. Invest. Dermatol. 92, 263-266, 1989
A;Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.
A;Reference number: A45910; MUID:89140394; PMID:2465353
A;Accession: A45910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <MCN>
A;Cross-references: UNIPROT:Q64526; GB:M27685; NID:g341749; PIDN:AAA81560.1; PID:g106681
C;Superfamily: ultra-high-sulfur keratin

Query Match 48.8%; Score 59; DB 2; Length 186;
Best Local Similarity 61.5%; Pred. No. 4.2; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2

Qy 4 YCCELCCYPACAG 16
Db 140 FCNLCCQPACSG 152

Search completed: March 26, 2005, 16:49:39
Job time : 3.81022 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:18 ; Search time 15.5036 Seconds
(without alignments)
594.533 Million cell updates/sec

Title: US-10-775-481A-3
Perfect score: 121
Sequence: 1 NTFYCCBLCCYPACAGCN 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	100.0	18	1 HSTB_ECOLI	P01560 escherichia
2	106	87.6	18	2 Q7M0U3	P01560 citrobacter
3	106	87.6	72	1 HST1_ECOLI	P01559 escherichia
4	98	81.0	61	2 Q6VEG9	Q6VEG9 escherichia
5	85	70.2	61	2 Q6VEG7	Q6VEG7 escherichia
6	85	70.2	61	2 Q6VEG8	Q6VEG8 escherichia
7	85	70.2	72	1 HST2_ECOLI	Q47185 escherichia
8	85	70.2	71	1 HST3_ECOLI	P74977 versinia en
9	83	68.6	71	1 HSTB_YEREN	P74977 versinia en
10	81	66.9	66	1 HST_YERKE	P31518 versinia kr
11	78	64.5	72	1 HSTC_YEREN	Q50319 versinia en
12	76	62.8	19	2 Q9R579	Q9R579 vibrio chol
13	76	62.8	28	2 Q9R578	Q9R578 vibrio chol
14	76	62.8	71	1 HSTA_YEREN	P07593 versinia en
15	76	62.8	78	1 HSTN_VIBCH	P04429 vibrio chol
16	76	62.8	78	1 HSTO_VIBCH	Q07425 vibrio chol
17	74	61.2	17	2 Q9R581	Q9R581 vibrio chol
18	74	61.2	18	2 Q9R580	Q9R580 vibrio chol
19	67	55.4	66	2 Q56643	Q56643 vibrio chol
20	65	53.7	78	2 Q93G01	Q93G01 vibrio mimi
21	63	52.1	107	1 GUAN_CAVPO	P70664 cavia porce
22	63	52.1	109	1 GUAN_PIG	P79897 sus scrofa
23	60	49.6	15	1 GUAN_DIDWA	P55936 didelphis m
24	60	49.6	105	2 Q9BYF8	Q9BYF8 homo sapien
25	59	48.8	115	1 GUAN_HUMAN	Q02747 homo sapien
26	59	48.8	115	1 GUAN_RAT	P28902 rattus norv
27	59	48.8	115	2 Q8R5G9	Q8R5G9 notomys ale
28	59	48.8	116	1 GUAN_MOUSE	P33680 mus musculu
29	59	48.8	186	2 Q64526	Q64526 mus musculu
30	59	48.8	191	2 Q9D3H7	Q9D3H7 mus musculu
31	59	48.8	195	2 Q9D141	Q9D141 mus musculu

32	57	47.1	370	2	Q96UR8	Q96ur8 laccaria bi
33	57	47.1	1043	2	Q9FNC3	Q9fnc3 arabidopsis
34	57	47.1	1049	2	Q84JA6	Q84ja6 arabidopsis
35	57	47.1	1055	2	Q8GZN8	Q8gzn8 arabidopsis
36	56	46.3	109	2	Q7ZS22	Q7zsz2 anguilla ja
37	56	46.3	179	2	Q88E38	Q88e38 aeromonas p
38	56	46.3	265	2	Q62149	Q62149 caenorhabdi
39	55	45.5	110	2	Q7ZS21	Q7zsz1 anguilla ja
40	55	45.5	167	2	Q9D122	Q9d122 mus musculu
41	54	44.6	118	2	Q8WTI6	Q8wti6 drosophila
42	54	44.6	690	2	Q95436	Q95436 homo sapien
43	53.5	44.2	152	2	Q9XVX3	Q9xvx3 caenorhabdi
44	53.5	44.2	164	2	Q22048	Q22048 caenorhabdi
45	53.5	44.2	166	2	Q95QY1	Q95qy1 caenorhabdi

ALIGNMENTS

RESULT 1
HSTB_ECOLI
ID HSTB_ECOLI STANDARD; PRT; 18 AA.
AC P01560;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin ST-2 (ST-B).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RC STRAIN=O42:K86:H37 / 18D / ETEC;
RX MEDLINE=81264141; PubMed=7021541;
RA Chan S.-K., Giannella R.A.;
RT "Amino acid sequence of heat-stable enterotoxin produced by
Escherichia coli pathogenic for man.";
RL J. Biol. Chem. 256:7744-7746(1981).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)90134-5;
RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (StH)
produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170(1987).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
cyclase and increases cyclic GMP levels within the host intestinal
epithelial cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
DR PIR; A01823; QHEC2.
DR HSPSP; P01559; IETN.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Direct protein sequencing; Enterotoxin; Toxin.
FT DISULFID 5 10
FT DISULFID 6 14
FT DISULFID 9 17
SQ SEQUENCE 18 AA; 1978 MW; D0C975F49D600650 CRC64;

Query Match 100.0%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NTFYCCBLCCYPACAGCN 18

Db 1 NTFYCCBLCCYPACAGCN 18

RESULT 2

```

Q7M0U3
ID Q7M0U3 PRELIMINARY; PRT; 18 AA.
AC Q7M0U3
DT 01-MAR-2004 (TReMBUrel. 26, Created)
DT 01-MAR-2004 (TReMBUrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBUrel. 26, Last annotation update)
DE Heat-stable enterotoxin ST-1a.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE.
RX MEDLINE=89108617; PubMed=2912902;
RA Guarino A., Giannella R., Thompson M.R.;
RT "Citrobacter freundii produces an 18-amino-acid heat-stable
RT enterotoxin identical to the 18-amino-acid Escherichia coli heat-
RL stable enterotoxin (ST 1a).";
RL Infect. Immun. 57:649-652(1989).
DR PIR; A60103; A60103.
DR HSP; P01559; LETN.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;

Query Match 87.6%; Score 106; DB 2; Length 18;
Best Local Similarity 94.1%; Pred. No. 9.7e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGC 17
DB 1 NTFYCCCLCCNPACGC 17

RESULT 3
HST1_ECOLI
ID HST1_ECOLI STANDARD; PRT; 72 AA.
AC P01559; Q47653;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Heat-stable enterotoxin ST-1A/ST-P precursor.
GN Name=stai;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Tn1681;
RX MEDLINE=81054703; PubMed=6254008;
RA So M., McCarthy B.J.;
RT "Nucleotide sequence of the bacterial transposon Tn1681 encoding a
RT heat-stable (ST) toxin and its identification in enterotoxigenic
RT Escherichia coli strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4011-4015(1980).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O42:H86:H37 / 18D / ETEC;
RX MEDLINE=90368614; PubMed=2203756;
RA Dallas W.S.;
RT "The heat-stable toxin I gene from Escherichia coli 18D.";
RL J. Bacteriol. 172:5490-5493(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85249571; PubMed=2990268;
RA Sekizaki T., Akashi H., Terakado N.;
RT "Nucleotide sequences of the genes for Escherichia coli heat-stable
RT enterotoxin I of bovine, avian, and porcine origins.";
RL Am. J. Vet. Res. 46:909-912(1985).

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[4]
RN DISULFIDE BONDS.
RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
RA Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)
RT produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170(1987).
RN [5]
RP PROCESSING.
RX MEDLINE=90368584; PubMed=2203746;
RA Okamoto K., Takahara M.;
RT "Synthesis of Escherichia coli heat-stable enterotoxin STp as a pre-
RT pro form and role of the pro sequence in secretion.";
RL J. Bacteriol. 172:5260-5265(1990).
RN [6]
RX X-RAY CRYSTALLOGRAPHY (0.89 ANGSTROMS) OF 59-71.
RA Sato T., Ozaki H., Hata Y., Kitagawa Y., Katsube Y., Shimonishi Y.;
RT "Structural characteristics for biological activity of heat-stable
RT enterotoxin produced by enterotoxigenic Escherichia coli: X-ray
RT crystallography of weakly toxic and nontoxic analogs.";
RL Biochemistry 33:8641-8650(1994).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; V00612; CAA23883.1; -
DR EMBL; M58746; AAA62776.1; -
DR EMBL; M25607; AAA24853.1; -
DR PIR; A01822; QHEC1.
DR PDB; 1ETL; X-ray; @=59-71.
DR PDB; 1ETM; X-ray; @=-.
DR PDB; 1ETN; X-ray; @=-.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW 3D-structure; Enterotoxin; Signal; Toxin; Transposable element.
FT SIGNAL 1 19
FT PROPEP 20 54 Heat-stable enterotoxin ST-1A/ST-P.
FT PEPTIDE 55 72
FT DISULFID 59 64
FT DISULFID 60 68
FT DISULFID 63 71
FT CONFLICT 70 70 G -> P (in Ref. 3).
FT TURN 61 62
FT TURN 66 67
FT TURN 69 70
SQ SEQUENCE 72 AA; 8075 MW; 92E8B766B3988264 CRC64;

Query Match 87.6%; Score 106; DB 1; Length 72;
Best Local Similarity 94.1%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTFYCCCLCCYPACAGC 17
DB 55 NTFYCCCLCCNPACAGC 71

RESULT 4
Q6VEG9 PRELIMINARY; PRT; 61 AA.
ID Q6VEG9
AC Q6VEG9;

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```
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Heat-stable enterotoxin ST-Ia (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F7682;
RX PubMed=15364995;
RA Reischl U., Yousef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
of heat-labile I and heat-stable I enterotoxin genes from
enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL: AY342057; AAQ92974.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR001489; Enterotoxin HS.
DR Pfam: PF02048; Enterotoxin HS; 1.
FT NON TER 1
SQ SEQUENCE 61 AA; 6927 MW; 646D4AE2F899D957 CRC64;

Query Match 81.0%; Score 98; DB 2; Length 61;
Best Local Similarity 88.2%; Pred. No. 2.6e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGC 17
| | | | | | | | | | | | | | | |
Db 44 NTFYCCCLCCNPACAPC 60

RESULT 5
Q6VEG7 PRELIMINARY; PRT; 61 AA.
AC Q6VEG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Heat-stable enterotoxin ST Ib (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R544;
RX PubMed=15364995;
RA Reischl U., Yousef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
of heat-labile I and heat-stable I enterotoxin genes from
enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL: AY342059; AAQ92976.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR001489; Enterotoxin HS.
DR Pfam: PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
FT NON TER 1
SQ SEQUENCE 61 AA; 6556 MW; 89788D3FAB3DCA0A CRC64;

Query Match 70.2%; Score 85; DB 2; Length 61;
Best Local Similarity 85.7%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YCCELCCYPACAGC 17
| | | | | | | | | | | | | | | |
Db 47 YCCELCCNPACTGC 60

RESULT 6
Q6VEG8 PRELIMINARY; PRT; 61 AA.
AC Q6VEG8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Heat-stable enterotoxin ST Ib (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C4046;
RX PubMed=15364995;
RA Reischl U., Yousef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
of heat-labile I and heat-stable I enterotoxin genes from
enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL: AY342058; AAQ92975.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR001489; Enterotoxin HS.
DR Pfam: PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
FT NON TER 1
SQ SEQUENCE 61 AA; 6658 MW; 1D75955D7AF0DED2 CRC64;

Query Match 70.2%; Score 85; DB 2; Length 61;
Best Local Similarity 85.7%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YCCELCCYPACAGC 17
| | | | | | | | | | | | | | | |
Db 47 YCCELCCNPACTGC 60

RESULT 7
HST2_ECOLI STANDARD; PRT; 72 AA.
ID_HST2_ECOLI STANDARD; PRT; 72 AA.
AC Q47185;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin A2 precursor (STA2).
GN Name=sta2;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89108616; PubMed=2643580;
RA Guzman-Verdugo L.M., Kupersztosch Y.M.;
RT "Rectification of two Escherichia coli heat-stable enterotoxin allele
sequences and lack of biological effect of changing the carboxy-
terminal tyrosine to histidine.";
RT Infect. Immun. 57:645-648(1989).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
cyclase and increases cyclic GMP levels within the host intestinal
epithelial cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC EMBL; M18345; AAA23729.1; -
DR PIR; JS0292; QHECIB.
DR HSSP; P01559; 1ETN.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 53 By similarity.
FT PEPTIDE 54 72 Heat-stable enterotoxin A2.
FT DISULFID 59 64 By similarity.
FT DISULFID 60 68 By similarity.
FT DISULFID 63 71 By similarity.
SQ SEQUENCE 72 AA; 7895 MW; D87850306E06B260 CRC64;

Query Match 70.2%; Score 85; DB 1; Length 72;
Best Local Similarity 85.7%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YCCELCCVPACAGC 17
Db 58 YCCELCCNPACTGC 71

RESULT 8
HST3_ECOLI STANDARD; PRT; 72 AA.
ID _HST3_ECOLI STANDARD; PRT; 72 AA.
AC P07955; P26588;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin A3/A4 precursor (STA3/STAA) (ST-IB) (ST-H).
GN Name:sta3; Synonyms:sta4;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89202548; PubMed=3071819;
RA Sieglitz H., Cervantes L., Robledo R., Fonseca R., Covarrubias L.,
RA Bolivar F., Kupersztoch Y.M.;
RT "Cloning, sequencing, and expression in Ficol-generated minicells of
RT an Escherichia coli heat-stable enterotoxin gene.";
RL Plasmid 20:42-53(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=153837-2;
RX MEDLINE=89202548; PubMed=3071819;
RA Sieglitz H., Cervantes L., Robledo R., Fonseca R., Covarrubias L.,
RA Bolivar F., Kupersztoch Y.M.;
RT "Cloning, sequencing, and expression in Ficol-generated minicells of
RT an Escherichia coli heat-stable enterotoxin gene.";
RL Plasmid 20:42-53(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89108616; PubMed=2643580;
RA Moseley S.L., Hardy J.W., Huq M.I., Echeverria P., Falkow S.;
RA Zhou X., Shen L.P., Chi C.W.;
RT "Isolation and nucleotide sequence determination of a gene encoding a
RT heat-stable enterotoxin of Escherichia coli.";
RL Infect. Immun. 39:1167-1174(1983).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90273381; PubMed=2190361; DOI=10.1016/0041-0101(90)90085-L;
RA Zhou X., Shen L.P., Chi C.W.;
RT "Isolation and nucleotide sequence determination of a gene encoding a
RT heat-stable enterotoxin of Escherichia coli.";
RL Toxicon 28:453-456(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=89108616; PubMed=2643580;
RA Guzman-Verduzo L.M., Kupersztoch Y.M.;
RT "Rectification of two Escherichia coli heat-stable enterotoxin allele
RT sequences and lack of biological effect of changing the carboxy-
RT terminal tyrosine to histidine.";
RL Infect. Immun. 57:645-648(1989).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=90034194; PubMed=2680769; DOI=10.1016/0378-1119(89)90182-0;
RA Dwarakanath P., Visweswariah S.S., Subrahmanyam Y.V.B.K., Shanthi G.,

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RA Jagannatha H.M., Balganes T.S.;
RT "Cloning and hyperexpression of a gene encoding the heat-stable toxin
RT of Escherichia coli.";
RL Gene 81:219-226(1989).
RN [6]
RP SEQUENCE OF 54-72.
RX MEDLINE=83105138; PubMed=6759126;
RA Aimoto S., Takao T., Shimonishi Y., Hara S., Takeda T., Takeda Y.,
RA Miwatani T.;
RT "Amino-acid sequence of a heat-stable enterotoxin produced by human
RT enterotoxigenic Escherichia coli.";
RL Eur. J. Biochem. 129:257-263(1982).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
RA Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (Sth)
RT produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:163-170(1987).
RN [8]
RP PROCESSING.
RX MEDLINE=90251166; PubMed=2187146;
RA Rasheed J.K., Guzman-Verduzo L.M., Kupersztoch Y.M.;
RT "Two precursors of the heat-stable enterotoxin of Escherichia coli:
RT evidence of extracellular processing.";
RL Mol. Microbiol. 4:265-273(1990).
CC CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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CC CC EMBL; J03311; AAA24652.1; -
DR EMBL; M34916; AAA23990.1; -
DR EMBL; M18346; AAA23730.1; -
DR EMBL; M29255; AAA24686.1; -
DR PIR; JS0292; QHECIB.
DR PIR; JT0373; QHEC4.
DR HSSP; P01559; 1ETN.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19
FT PROPEP 20 53 Heat-stable enterotoxin A3/A4.
FT PEPTIDE 54 72
FT DISULFID 59 64
FT DISULFID 60 68
FT DISULFID 63 71
FT CONFLICT 19 19 A -> P (in Ref. 2).
SQ SEQUENCE 72 AA; 7909 MW; 1C5C9292BFCBA6BA CRC64;

Query Match 70.2%; Score 85; DB 1; Length 72;
Best Local Similarity 85.7%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YCCELCCVPACAGC 17
Db 58 YCCELCCNPACTGC 71

RESULT 9
HSTB_YEREN STANDARD; PRT; 71 AA.
ID _HSTB_YEREN STANDARD; PRT; 71 AA.

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AC P74977;
DT 15-DEC-1998 (Rel. 37, Created)
DE 05-JUL-2004 (Rel. 44, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin B precursor (Y-STB).
GN Name=YstB;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=84-50 / Serotype O:5;
RX MEDLINE=98008784; PubMed=9344780; DOI=10.1006/mpat.1997.0146;
RA Ramamurthy T., Yoshino K., Huang X., Nair G.B., Carniel E.,
RA Maruyama T., Fukushima H., Takeda T.;
RT "The novel heat-stable enterotoxin subtype gene (ystB) of Yersinia
RT enterocolitica: nucleotide sequence and distribution of the yst
RT genes."; Pathog. 23:189-200(1997).
RL Microb. Pathog. 23:189-200(1997).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells. Could play an important role in pathogenesis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC
CC EMBL; D88145; BAAL3544.1; -
CC HSPF; P01559; IETN.
CC InterPro; IPR001489; Enterotoxin HS.
CC Pfam; PF02048; Enterotoxin HS; 1.
CC PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
CC Direct protein sequencing; Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 52
FT CHAIN 53 71 Heat-stable enterotoxin B.
FT DISULFID 59 64 By similarity.
FT DISULFID 60 68 By similarity.
FT DISULFID 63 71 By similarity.
SQ SEQUENCE 71 AA; 7670 MW; ED6E9F61ACDD4F50 CRC64;

Query Match 68.6%; Score 83; DB 1; Length 71;
Best Local Similarity 70.6%; Pred. No. 0.0023;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGC 17
Db 55 NDDWCCEVCNCPACAGC 71

RESULT 10
HST_YERKR
ID HST_YERKR STANDARD; PRT; 66 AA.
AC P31518;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin precursor.
GN Name=Yst;
OS Yersinia kristensenii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=28152;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP490 / Serotype O:12,25;

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RA Ibrahim A., Liesack W., Stackebrandt E.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC
CC EMBL; X69218; CAA49152.1; -
CC PIR; S31652; S31652.
CC HSPF; P01559; IETN.
CC InterPro; IPR001489; Enterotoxin HS.
CC Pfam; PF02048; Enterotoxin HS; 1.
CC PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
CC Enterotoxin; Signal.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 50
FT CHAIN 51 66 Heat-stable enterotoxin (By similarity).
FT DISULFID 54 59 By similarity.
FT DISULFID 55 63 By similarity.
FT DISULFID 58 66 By similarity.
SQ SEQUENCE 66 AA; 7068 MW; 27BE7006675CC075 CRC64;

Query Match 66.9%; Score 81; DB 1; Length 66;
Best Local Similarity 78.6%; Pred. No. 0.0038;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YCCELCYCPACAGC 17
Db 53 WCCEVCNCPACAGC 66

RESULT 11
HSTC_YEREN
ID HSTC_YEREN STANDARD; PRT; 72 AA.
AC O50319;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin C precursor (Y-STC).
GN Name=YstC;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-11;
RX MEDLINE=97202479; PubMed=9049998; DOI=10.1006/mpat.1996.0094;
RA Huang X., Yoshino K., Nakao H., Takeda T.;
RT "Nucleotide sequence of a gene encoding the novel Yersinia
RT enterocolitica heat-stable enterotoxin that includes a pro-region-like
RT sequence in its mature toxin molecule.";
RL Microb. Pathog. 22:89-97(1997).
RN [2]
RP SEQUENCE OF 20-72.
RC STRAIN=Serotype O:3;
RX MEDLINE=95246844; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
RA Yoshino K., Takao T., Huang X., Murata H., Nakao H., Takeda T.,
RA Shimomishi Y.;
RT "Characterization of a highly toxic, large molecular size heat-stable
RT enterotoxin produced by a clinical isolate of Yersinia
RT enterocolitica.";
RN FEBS Lett. 362:319-322(1995).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate

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CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells. Highly toxic.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC
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DR EMBL; D63578; BAA23656.1; --
 DR HSSP; P01559; IETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
 FT SIGNAL 1 19
 FT CHAIN 20 72 Heat-stable enterotoxin C.
 FT DISULFID 60 65 By similarity.
 FT DISULFID 61 69 By similarity.
 FT DISULFID 64 72 By similarity.
 SQ SEQUENCE 72 AA; 7639 MW; 7C0D83893C2F981D CRC64;

Query Match 64.5%; Score 78; DB 1; Length 72;
 Best Local Similarity 78.6%; Pred. No. 0.0096;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YCELCYCPACGC 17
 :|||||
 Db 59 WCCELCNCPACGCG 72

RESULT 12

Q9R579 Q9R579 PRELIMINARY; PRT; 19 AA.
 AC Q9R579;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 01-ST-3=HEAT-stable enterotoxin.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
 RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
 RA Takeda T., Shimonishi Y.;
 RT "Purification and sequence determination of heat-stable enterotoxin
 RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
 RT Ol.",
 RL FEBS Lett. 326:83-86(1993).
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 SQ SEQUENCE 19 AA; 2048 MW; 308015F1A18D601C CRC64;

Query Match 62.8%; Score 76; DB 2; Length 19;
 Best Local Similarity 64.7%; Pred. No. 0.0058;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 NTFYCELCYCPACGC 17
 :|||||
 Db 1 NLIDCCNCPACGCG 17

RESULT 13

Q9R578 Q9R578 PRELIMINARY; PRT; 28 AA.
 AC Q9R578;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 01-ST-4=HEAT-stable enterotoxin.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
 RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
 RA Takeda T., Shimonishi Y.;
 RT "Purification and sequence determination of heat-stable enterotoxin
 RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
 RT Ol.",
 RL FEBS Lett. 326:83-86(1993).
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 SQ SEQUENCE 28 AA; 3080 MW; 25ECADAF5C57DB72 CRC64;

Query Match 62.8%; Score 76; DB 2; Length 28;
 Best Local Similarity 64.7%; Pred. No. 0.0079;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 NTFYCELCYCPACGC 17
 :|||||
 Db 10 NLIDCCNCPACGCG 26

RESULT 14

HSTA YEREN
 ID HSTA YEREN STANDARD; PRT; 71 AA.
 AC P07593;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin A precursor (VST-A).
 GN Name=VstA; Synonyms=vst;
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Serotype O:8;
 RX MEDLINE=93051243; PubMed=1427005; DOI=10.1016/0378-1097(92)90364-T;
 RA Ibrahim A., Liesack W., Pike S., Stackebrandt E.;
 RT "The polymerase chain reaction: an epidemiological tool to
 RT differentiate between two clusters of pathogenic Yersinia
 RT enterocolitica strains";
 RL FEMS Microbiol. Lett. 76:63-66(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W1024 / Serotype O:9;
 RX MEDLINE=90354067; PubMed=2201642;
 RA Delor I., Kaeckenbeek A., Wauters G., Cornelis G.R.;
 RT "Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding
 RT the heat-stable enterotoxin, and prevalence of the gene among
 RT pathogenic and nonpathogenic yersiniae";
 RL Infect. Immun. 58:2983-2988(1990).
 RN [3]
 RP SEQUENCE OF 54-71.
 RX MEDLINE=86004705; PubMed=4043080;
 RA Takao T., Tominega N., Yoshimura S., Shimonishi Y., Hara S., Inoue T.,
 RA Miyama A.;
 RT "Isolation, primary structure and synthesis of heat-stable enterotoxin

RT produced by *Yersinia enterocolitica*.";
 RL -J. F. Blochem. 152:199-206(1985).
 CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- INDUCTION: In cultured cells, expressed only at temperatures <30
 CC degrees Celsius. Under conditions of high osmolarity and alkaline
 CC pH (as it is the case in the host's intestine), it is expressed at
 CC 37 degrees Celsius.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC
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 CC
 DR EMBL; X65999; CAA46801.1; -;
 DR EMBL; U09235; AAA18472.1; -;
 DR PIR; S25659; S25659.
 DR HSP; P01559; LETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 DR Direct protein sequencing; Enterotoxin; Signal; Toxin.
 KW SIGNAL 1 19 Potential.
 FT PROPEP 20 53
 FT CHAIN 54 71 Heat-stable enterotoxin A.
 FT DISULFID 59 64 By similarity.
 FT DISULFID 60 68 By similarity.
 FT DISULFID 63 71 By similarity.
 FT VARIANT 48 48 L->S
 SQ SEQUENCE 71 AA; 7494 MW; 022F99B3800C861B CRC64;
 Query Match 62.8%; Score 76; DB 1; Length 71;
 Best Local Similarity 76.9%; Pred. No. 0.017;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 CCELCVCPACAGC 17
 Db 59 CCDVCCNPACAGC 71
 |||:|||||
 RESULT 15
 ID HSTN_VIBCH STANDARD; PRT; 78 AA.
 AC P04429;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin ST precursor (Nonagglutinating cholera vibrios
 DE ST) (NAG-ST) (Non O1-ST).
 GN Name=stn;
 OS *Vibrio cholerae*, and
 OS *Vibrio mimicus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=666, 674;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=*V. cholerae*; STRAIN=NRT36;
 RA MEDLINE=90382953; PubMed=2205577;
 RA Ogawa A., Kato J.I., Watanabe H., Nair B.G., Takeda T.;
 RT "Cloning and nucleotide sequence of a heat-stable enterotoxin gene
 RT from *Vibrio cholerae* non-O1 isolated from a patient with traveler's
 RT diarrhea.";
 RL Infect. Immun. 58:3325-3329(1990).
 RN [2]
 RP SEQUENCE OF 62-78.
 RC SPECIES=*V. cholerae*; STRAIN=Seroovar non-O1;

RX MEDLINE=86056320; PubMed=4065341; DOI=10.1016/0014-5793(85)80163-0;
 RA Takao T., Shimonishi Y., Kobayashi M., Nishimura O., Arita M.,
 RA Takeda T., Honda T., Miwatani T.;
 RT "Amino acid sequence of heat-stable enterotoxin produced by *Vibrio*
 RT *cholerae* non-O1.";
 RL FEBS Lett. 193:250-254 (1985).
 RN [3]
 RN SEQUENCE OF 62-78.
 RP SPECIES=*V. mimicus*; STRAIN=AQ-0915;
 RC MEDLINE=91257548; PubMed=2044934; DOI=10.1016/0378-1097(91)90536-J;
 RX Arita M., Honda T., Miwatani T., Takeda T., Takao T., Shimonishi Y.;
 RA "Purification and characterization of a heat-stable enterotoxin of
 RT *Vibrio mimicus*.";
 RL FEBS Microbiol. Lett. 63:105-110(1991).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 DR EMBL; M85198; AAA64889.1; -;
 DR PIR; A41469; QHVC1.
 DR HSP; P01559; LETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 DR Direct protein sequencing; Enterotoxin; Signal; Toxin.
 KW SIGNAL 1 18 Potential.
 FT PROPEP 19 61
 FT CHAIN 62 78 Heat-stable enterotoxin ST.
 FT DISULFID 64 69 By similarity.
 FT DISULFID 65 73 By similarity.
 FT DISULFID 68 76 By similarity.
 SQ SEQUENCE 78 AA; 8830 MW; EED385B298D0964F CRC64;
 Query Match 62.8%; Score 76; DB 1; Length 78;
 Best Local Similarity 64.7%; Pred. No. 0.018;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 NTFYCCBLCCVCPACAGC 17
 Db 60 NLIDCCBLCCNPACFCG 76
 |||:|||||
 Search completed: March 26, 2005, 16:48:34
 Job time : 16.5037 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 26, 2005, 17:26:07 ; Search time 90.5 Seconds
(without alignments)
487.190 Million cell updates/sec

Title: US-10-775-481A-4
Perfect score: 126
Sequence: 1 aatagtagcaattactgtg.....ctgtgttaacgggtgctat 57

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USFNO.spool_p/US1075481/runat_25032005.151017.7781/app.query.fasta_1.199
-DB=A_Geneseq_16Dec04 -QWTF=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US1075481.CG 1.154 @runat_25032005.151017.7781 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	19	2 AAR85948	AAR85948 ST Ib rec
2	126	100.0	19	2 AAY40510	Aay40510 ST recept
3	126	100.0	19	8 ADR45825	Adr45825 Amino aci
4	120	95.2	19	2 AAR95923	Aar95923 Enterotox
5	120	95.2	19	2 AAY02386	Aay02386 Heat stab
6	120	95.2	19	2 AAY29608	Aay29608 Escherich
7	120	95.2	19	2 AAY06972	Aay06972 E. coli h
8	120	95.2	19	2 AAY02398	Aay02398 Heat stab
9	120	95.2	19	4 AAM51879	Aam51879 Human the
10	120	95.2	19	6 AAO16204	Aao16204 E coli sm

11	120	95.2	19	6 ABG74825	Abg74825 E. coli h
12	120	95.2	19	7 ADC14120	Adc14120 Heat stab
13	120	95.2	19	8 ADR48340	Adr48340 Bacterial
14	120	95.2	19	8 ADR48359	Adr48359 Analgesic
15	120	95.2	19	8 ADR48398	Adr48398 Peptide u
16	120	95.2	19	8 ADR48329	Adr48329 E. coli S
17	120	95.2	21	8 ADR48372	Adr48372 Analgesic
18	120	95.2	21	8 ADR48413	Adr48413 GC-C acti
19	120	95.2	72	2 AAR20352	Aar20352 Sequence
20	120	95.2	72	2 AAR71975	Aar71975 E. coli s
21	120	95.2	72	8 ADR48356	Adr48356 Immature
22	118	93.7	19	8 ADR48451	Adr48451 GC-C acti
23	118	93.7	19	8 ADR48453	Adr48453 GC-C acti
24	118	93.7	19	8 ADR48302	Adr48302 GC-C acti
25	118	93.7	19	8 ADR48304	Adr48304 GC-C acti
26	117	92.9	19	8 ADR48310	Adr48310 GC-C acti
27	117	92.9	19	8 ADR48459	Adr48459 GC-C acti
28	116	92.1	19	7 ADC14123	Adc14123 Modified
29	116	92.1	19	7 ADC14121	Adc14121 Modified
30	116	92.1	19	8 ADR48360	Adr48360 Analgesic
31	116	92.1	19	8 ADR48305	Adr48305 GC-C acti
32	116	92.1	19	8 ADR48454	Adr48454 GC-C acti
33	116	92.1	19	8 ADR48404	Adr48404 GC-C acti
34	116	92.1	21	8 ADR48415	Adr48415 GC-C acti
35	116	92.1	21	8 ADR48373	Adr48373 Analgesic
36	116	92.1	21	8 ADR48374	Adr48374 Analgesic
37	116	92.1	21	8 ADR48414	Adr48414 GC-C acti
38	115	91.3	19	4 AAB83216	Aab83216 Escherich
39	115	91.3	19	8 ADR48446	Adr48446 GC-C acti
40	115	91.3	19	8 ADR48361	Adr48361 Analgesic
41	115	91.3	19	8 ADR48442	Adr48442 GC-C acti
42	115	91.3	19	8 ADR48293	Adr48293 GC-C acti
43	115	91.3	19	8 ADR48401	Adr48401 Peptide u
44	115	91.3	19	8 ADR48297	Adr48297 GC-C acti
45	115	91.3	19	8 ADR48308	Adr48308 GC-C acti

ALIGNMENTS

RESULT 1
AAR85948
ID AAR85948 standard; peptide; 19 AA.
XX
AC AAR85948;
XX
XX
DT 19-JAN-1996 (first entry)
XX
XX ST Ib receptor ligand portion.
DE
XX ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
KW colorectal; metastasis.
XX
XX Escherichia coli.
XX
XX WO9511694-A1.
PN
XX
PD 04-MAY-1995.
XX
XX 26-OCT-1994; 94WO-US012232.
PF
XX 26-OCT-1993; 93US-00141892.
PR 13-SEP-1994; 94US-00305056.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
PA
XX Waldman SA;
XX
XX WPI; 1995-178646/23.
XX
XX Conjugated cpds. which specifically bind to colorectal cancer cells -
PT comprise heat-stable toxin receptor binding moiety and active moiety
PT which may be a therapeutic agent or a radioactive agent.
XX

PS Claim 3; Page 116; 133pp; English.

XX New conjugated compounds are provided which consist of (1) an ST receptor
CC binding moiety and (2) an active moiety which is a radio-stable agent.
CC 'ST' refers to a heat stable toxin produced by E.coli and other
CC organisms. Especially the radiostable agent is a therapeutic agent (e.g.
CC methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive
CC isotope) or nucleic acid; and the compound is used for the detection,
CC imaging or treatment of colorectal tumours, particularly metastasised
CC tumours. The present sequence is a specific example of an ST receptor
CC binding peptide which can be used in the conjugate

XX Sequence 19 AA;

Alignment Scores:
Pred. No.: 1.36e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x AAR85948 (1-19)

Qy 1 AATAGTACCAATCTGCTGTAATGTTGTAATCTGCTGTAACGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 2

AY40510
ID AY40510 standard; peptide; 19 AA.

XX AC AY40510;

DT 03-DEC-1999 (first entry)

DE ST receptor peptide ST lb.

XX Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.

XX Escherichia coli.

XX US962220-A.

XX 05-OCT-1999.

XX 06-JUN-1995; 95US-00467920.

XX 26-OCT-1993; 93US-00141892.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Waldman SA;

XX WPI; 1999-571264/48.

XX N-PSDB; AA207541.

XX Conjugated compound comprising a receptor moiety and active moiety,
PT useful for the treatment/prevention of colorectal cancer.

XX Claim 1; Col 21-22; 23pp; English.

XX The invention relates to a conjugated compound that comprises a ST (heat-
CC stable toxin) receptor moiety selected from one of the sequences shown in
CC AY40508-Y40559 and an active moiety (antisense molecule). The compound
CC is useful for the treatment of colorectal cancer. The use of the
CC conjugated compound is advantageous compared to antibodies since it binds
CC specifically to colorectal cells and has no toxic effect on normal cells.
CC The present sequence represents the amino acid sequence of a ST receptor
CC peptide ST lb

XX Sequence 19 AA;

Alignment Scores:

Pred. No.: 1.36e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x AAY40510 (1-19)

Qy 1 AATAGTACCAATCTGCTGTAATGTTGTAATCTGCTGTAACGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 3

ADR45825

ID ADR45825 standard; peptide; 19 AA.

XX AC ADR45825;

XX DT 18-NOV-2004 (first entry)

XX Amino acid sequence of heat stable toxin ST lb.

XX heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
KW ST lb.

XX Unidentified.

XX WO2004071436-A2.

XX 26-AUG-2004.

XX 10-FEB-2004; 2004WO-US003765.

XX 10-FEB-2003; 2003US-0446730P.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;
DR WPI; 2004-615913/59.

XX N-PSDB; ADR45824.

XX Increasing ST receptor molecules on the surface of a colorectal, gastric
PT or esophageal cancer cell to treat these cancers comprises administering
PT ST receptor ligand molecules that bind to ST receptors on the surface of
PT the cancer cell.

XX Claim 6; SEQ ID NO 5; 97pp; English.

XX The specification describes a method for increasing the number of heat
CC stable toxin (ST) receptor molecules on the surface of a metastasised
CC colorectal cancer cell. The method comprises administering, by continuous
CC infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
CC per hour for at least 6 hours, where ST receptor ligand molecules bind to
CC ST receptors on the surface of the cancer cell in the individual and the
CC number of ST receptor molecules on the surface of the cancer cell is
CC increased. Therapeutic compositions comprising components which target ST
CC receptors can then be used to inhibit proliferation of the colorectal,
CC gastric and oesophageal cells. This method may be used for treating
CC individuals that have diseases that affect colorectal, gastric and
CC oesophageal cells, including colorectal, gastric or oesophageal cancers.
CC The present sequence represents a ST, designated ST lb, which is used as
CC the ST receptor ligand in the method of the invention.

XX Sequence 19 AA;

Alignment Scores:

Pred. No.: 1.36e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0

```

RESULT 5
AA020386
ID ID
XX AA020386 standard; peptide; 19 AA.
XX AC
XX AAY02386;
XX DT
XX 09-JUL-1999 (first entry)
XX DE
XX Heat stable ST enterotoxin Sth.
XX KW
XX Selection; candidate drug; cell receptor binding; affinity;
XX KW biological receptor; rational drug design; combinatorial drug design;
XX KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
XX KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
XX OS
XX Escherichia coli.
XX PN
XX W09909416-A2.
XX PD
XX 25-FEB-1999.
XX PF
XX 20-AUG-1998; 98WO-GB002504.
XX PR
XX 20-AUG-1997; 97GB-00017652.
XX PA
XX (NYCO-) NYCOMED IMAGING AS.
XX PI
XX (COCK/) COCKBAIN J.
XX PI
XX Wolfe HR;
XX DR
XX WPI; 1999-181156/15.
XX PT
XX Method of drug selection - and use of an acetamidomethyl-protected
XX PP polymer as a substrate in the solid state synthesis of an oligopeptide.
XX PS
XX Disclosure; Page 1-2; 38pp; English.
XX CC
XX The specification describes a method for selecting a candidate drug
XX CC compound having affinity for biological receptors. The method uses a
XX CC combination of rational and combinatorial drug design techniques. At
XX CC least 1 residue in the original cell receptor binding peptide is modified
XX CC to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
XX CC mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method
XX CC is used for identification of a candidate receptor antagonist or agonist.
XX CC The present peptide is a cell receptor binding peptide, and can thus be
XX CC used as a starting point for identification of candidate drug compounds,
XX CC using the method of the invention
XX SQ
XX Sequence 19 AA;

Alignment Scores:
Pred. No.: 8.79e-08 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: Gaps: 0

US-10-775-481A-4 (1-57) x AAY02386 (1-19)

QY 1 AATAGTAGCAATTAAGTCTGTGAATTTGTTGTAATCTCGTTGTAAACGGTGCTAT 57
Db 1 AenSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 6
AAY29608
ID ID
XX AA029608 standard; peptide; 19 AA.
XX AC
XX AAY29608;
XX DT
XX 15-OCT-1999 (first entry)
XX DE
XX Escherichia coli heat stable ST enterotoxin Sth.

```

XX Heat stable ST enterotoxin; immunoreagent; radiological therapy;
 KW diagnosis; ST receptor binding moiety; macrocyclic complexing agent;
 KW tumour; infectious diarrhoeal disease; diarrhoea.
 XX
 OS Escherichia coli.
 XX
 PN WO9939748-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 08-FEB-1999; 99WO-GB000396.
 XX
 PR 06-FEB-1998; 98US-00020233.
 XX
 PA (NYCO-) NYCOMED IMAGING AS.
 PA (MATT/) MATTHEWS D P.
 XX
 PI Snow RA, Delecki DJ, Shah C, Black C, Wolfe H;
 XX WPI; 1999-494219/41.
 DR
 XX
 PT Macrocyclic complexing agents containing linked 2,6-pyridinylene nuclei
 PT as components of targeting immunoreagents binding to ST receptor.
 XX
 PS Disclosure; Page 39; 79pp; English.
 XX
 CC The present invention describes targeting immunoreagents (TI's)
 CC comprising a metal ion and a residue of a macrocyclic complexing agent
 CC (MCA). TI's are of use in diagnostic imaging and therapy of specific
 CC disease sites in a patient, using either radioactive, magnetic resonance,
 CC or fluorescent means of detection or use of the metal ion; alternatively,
 CC a substituent of these types may be introduced, e.g. radioactive iodine,
 CC to perform the same function. Most notable is the imaging and
 CC radiological therapy of tumours. In addition, a variety of bacteria,
 CC including Escherichia coli, Vibrio cholerae, Citrobacter freundii, and
 CC Yersinia enterocolitica, bind to ST receptors and cause infectious
 CC diarrhoeal diseases, particularly in pediatrics and in developing
 CC countries. These types of diarrhoea can also be treated using TI's. TI's
 CC may specifically used to treat cancers and also be used as an
 CC anti-diarrhoeal agent. TI's are free from the various disadvantages of
 CC prior art reagents, including rapid destruction and/or excretion,
 CC instability in storage, and protein degradation. There is no perturbation
 CC of protein reactive groups at the pyridyl chelating site. AAY29607 to
 CC AAY29612 represent examples of heat stable ST enterotoxins given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 AA;
 Alignment Scores:
 Pred. No.: 8,79e-08 Length: 19
 Score: 120.00 Matches: 18
 Percent Similarity: 94.74% Conservative: 0
 Best Local Similarity: 94.74% Mismatches: 1
 Query Match: 95.24% Indels: 0
 DB: 2 Gaps: 0
 US-10-775-481A-4 (1-57) x AAY29608 (1-19)
 QY 1 AATAGTAGCAATTAAGTCTGCTGTAATTTGTTGTAATCTGCTTGTACGGTGCTAT 57
 Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19
 RESULT 7
 AAY06972
 ID AAY06972 standard; peptide; 19 AA.
 XX
 AC AAY06972;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE E. coli heat stable ST enterotoxin peptide Sth.
 XX

KW Targeting immunoreagent; metal ion; immunoreactive; terpyridine; tumour;
 KW complexing agent; diagnostic imaging; radiological treatment; yttrium;
 KW therapeutic; radiation toxicity; heat stable; ST enterotoxin.
 XX
 OS Escherichia coli.
 XX
 PN WO9921587-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 15-OCT-1998; 98WO-GB003102.
 XX
 PR 15-OCT-1997; 97US-00951144.
 XX
 PA (NYCO-) NYCOMED IMAGING AS.
 PA (MATT/) MATTHEWS D P.
 XX
 PI Wolfe H, Delecki DJ, Yu S;
 XX WPI; 1999-302905/25.
 DR
 XX
 PT Targeting immunoreagent for diagnostic imaging and therapeutic
 PT compositions.
 XX
 PS Claim 16; Page 50; 57pp; English.
 XX
 CC The invention provides a targeting immunoreagent that comprises a metal
 CC ion and an immunoreactive group covalently bonded to a terpyridine
 CC complexing agent of a specified formula. The immunoreagent is useful in
 CC diagnostic imaging and therapeutic compositions. The immunoreagent is
 CC used for radiological treatment of tumours. When the immunoreagent
 CC contains yttrium, the radiation toxicity is lower compared with other
 CC yttrium chelators. The immunoreagent is not rapidly metabolized and does
 CC not disperse and efficiently forms covalent bonds with proteins and other
 CC biological molecules. The immunoreagent has good emission characteristics
 CC and are easily spectrophotometrically analysed. Protein conjugates can be
 CC stored for metal complexing without activation steps that degrade
 CC protein. The terpyridine complexing agent rapidly complex with metals and
 CC the obtained chelates have good stability. Sequences AAY06971-976
 CC represent examples of heat stable ST enterotoxin peptides that can be
 CC used as the immunoreactive group in the immunoreagent of the invention
 XX
 SQ Sequence 19 AA;
 Alignment Scores:
 Pred. No.: 8,79e-08 Length: 19
 Score: 120.00 Matches: 18
 Percent Similarity: 94.74% Conservative: 0
 Best Local Similarity: 94.74% Mismatches: 1
 Query Match: 95.24% Indels: 0
 DB: 2 Gaps: 0
 US-10-775-481A-4 (1-57) x AAY06972 (1-19)
 QY 1 AATAGTAGCAATTAAGTCTGCTGTAATTTGTTGTAATCTGCTTGTACGGTGCTAT 57
 Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19
 RESULT 8
 AAY02398
 ID AAY02398 standard; peptide; 19 AA.
 XX
 AC AAY02398;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Heat stable ST enterotoxin Sth.
 XX
 KW Selection; candidate drug; cell receptor binding; affinity;
 KW biological receptor; rational drug design; combinatorial drug design;
 KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
 KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
 XX

```

OS Escherichia coli.
XX
PN WO9909417-A2.
XX
XX
PD 25-FEB-1999.
XX
XX
PF 20-AUG-1998; 98WO-GB002510.
XX
XX
PR 20-AUG-1997; 97GB-00017652.
XX
XX
PA (NYCO-) NYCOMED IMAGING AS.
PA (COCK/) COCKBAIN J.
XX
XX
PI Wolfe HR;
XX
XX
XX WPI; 1999-181157/15.
XX
XX
PT Method of drug selection - using a combination of rational and
PT combinatorial drug design techniques.
XX
XX
PS Disclosure; Page 1-2; 35pp; English.
XX
XX
CC The specification describes a method for selecting a candidate drug
CC compound having affinity for biological receptors. The method uses a
CC combination of rational and combinatorial drug design techniques. At
CC least 1 residue in the original cell receptor binding peptide is modified
CC to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
CC mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method
CC is used for identification of a candidate receptor antagonist or agonist.
CC The present peptide is a cell receptor binding peptide, and can thus be
CC used as a starting point for identification of candidate drug compounds,
CC using the method of the invention
XX
XX
SQ Sequence 19 AA;
XX
XX
Alignment Scores:
Pred. No.: 8.79e-08 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 2 Gaps: 0
XX
US-10-775-481A-4 (1-57) x AAY02398 (1-19)
XX
Qy 1 AATAGTACAAATTACTGCTGCAATTGCTTGAATCCTGCTGTAAACGGGTGCTAT 57
Db 1 AenSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19
XX
RESULT 9
AAMS1879
ID AAM51879 standard; peptide; 19 AA.
XX
AC AAMS1879;
XX
XX
DT 01-FEB-2002 (first entry)
XX
XX
DE Human thermostable enterotoxin STh peptide fragment #3.
XX
XX
KW Human; thermostable enterotoxin; STh; metastatic colorectal cancer;
KW guanyl cyclase-C; GC-C; STA.
XX
XX
OS Homo sapiens.
XX
XX
FN FR2805994-A1.
XX
XX
PD 14-SEP-2001.
XX
XX
PF 10-MAR-2000; 2000FR-00003141.
XX
XX
PR 10-MAR-2000; 2000FR-00003141.
XX
XX
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.

```

XX WPI; 2003-148251/14.

XX Novel guanylate cyclase receptor agonist peptide useful for preventing or

PT treating primary or metastatic cancer and polyyps in a patient, and for

PT inducing apoptosis in the cells of a subject.

XX

PS Disclosure; Page 10; 47pp; English.

XX

CC The invention comprises guanylate cyclase receptor agonist peptides that

CC are useful for inducing apoptosis in the cells of a subject. The peptides

CC of the invention may be used to treat: cancer; polyyps; inflammation;

CC asthma; nephritis; hepatitis; pancreatitis; bronchitis; cystic fibrosis;

CC inflammatory bowel disease; ulcerative colitis; Crohn's disease; and

CC Kaposi's sarcoma. The present amino acid sequence represents an

CC Escherichia coli small heat stable enterotoxin tricyclo peptide which was

CC used in the invention

XX

SQ Sequence 19 AA;

Alignment Scores:

Pred. No.:	8.79e-08	Length:	19
Score:	120.00	Matches:	18
Percent Similarity:	94.74%	Conservative:	0
Best Local Similarity:	94.74%	Mismatches:	1
Query Match:	95.24%	Indels:	0
DB:	6	Gaps:	0

US-10-775-481A-4 (1-57) x RAO16204 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTGAATTGTGTGTAATCCTGCTTGTAAACGGGTGCTAT 57

Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 11

ABG74825

ID ABG74825 standard; peptide; 19 AA.

AC ABG74825;

XX

XX 12-JUN-2003 (first entry)

DE E. coli heat stable enterotoxin derived peptide SEQ ID 7.

XX

KW Apical membrane; mucosal epithelial cell; respiratory tract;

KW guanylate cyclase C; G protein-coupled receptor; guanosine triphosphate;

KW cyclic guanosine monophosphate; cGMP; chloride ion secretion; inhalation;

KW membrane-associated type II protein kinase; mucus fluidisation;

KW cystic fibrosis transmembrane conductance regulator; breathing disorder;

KW mucus secretion; antiasthmatic; antiinflammatory; bronchial asthma;

KW chronic bronchitis; cystic fibrosis; enterotoxin; heat stable.

XX

OS Escherichia coli.

XX

PN WO200298912-A2.

XX

PD 12-DEC-2002.

XX

PF 05-JUN-2002; 2002WO-DE002040.

XX

PR 05-JUN-2001; 2001DE-01027119.

XX

PA (CETI/) CETIN Y.

PA (SAVA/) SAVAS Y.

XX

PI Cetin Y, Savas Y;

XX

XX WPI; 2003-156842/15.

XX

PT Composition useful for treating respiratory disease, comprises a peptide

PT that activates guanylate cyclase C, and is delivered to the apical

PT membrane through the respiratory tract.

XX

PS Claim 3; Page 4; 23pp; German.

XX

CC This invention describes a novel medicament in a formulation that is

CC delivered to the apical membrane of mucosal epithelial cells through the

CC respiratory tract. The medicament contains at least one peptide that

CC activates guanylate cyclase C (GCC). GCC is a G protein-coupled receptor

CC that catalyses conversion of guanosine triphosphate to cyclic guanosine

CC monophosphate (cGMP) and is present on the apical (air) side of

CC respiratory epithelial cells but not on the basolateral (blood) side.

CC cGMP activates membrane-associated type II protein kinase which in turn

CC activates the regulatory domain of the cystic fibrosis transmembrane

CC conductance regulator, resulting in secretion of chloride ions and water

CC from the cells, causing fluidisation of the mucus. The products of the

CC invention are used to make an inhalation device containing the medicament

CC for diagnosing diseases that are accompanied by breathing disorders or

CC disorders of mucus secretion in the respiratory tract, by detecting at

CC least one GCC activator. The products of the invention have antiasthmatic

CC and antiinflammatory activity. The method is useful for diagnosing and

CC treating diseases accompanied by breathing disorders or disorders of

CC mucus secretion in the respiratory tract particularly bronchial asthma,

CC chronic bronchitis and cystic fibrosis. The product of the invention

CC improves fluidity and evacuation of bronchial mucus and acts locally

CC (since the medicament does not enter the bloodstream), so systemic side

CC effects are minimised. Only very small doses of the medicament are

CC required. This sequence represents a heat stable E. coli enterotoxin

CC derived peptide use in an assay to determine guanylate cyclase C

CC activation described in the disclosure of the invention

XX

SQ Sequence 19 AA;

Alignment Scores:

Pred. No.:	8.79e-08	Length:	19
Score:	120.00	Matches:	18
Percent Similarity:	94.74%	Conservative:	0
Best Local Similarity:	94.74%	Mismatches:	1
Query Match:	95.24%	Indels:	0
DB:	6	Gaps:	0

US-10-775-481A-4 (1-57) x ABG74825 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTGAATTGTGTGTAATCCTGCTTGTAAACGGGTGCTAT 57

Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 12

ADC14120

ID ADC14120 standard; peptide; 19 AA.

XX

AC ADC14120;

XX

DT 18-DEC-2003 (first entry)

XX

DE Heat stable enterotoxin, STH.

XX

KW Breast cancer; prostate cancer; pancreatic cancer; melanoma;

KW heat stable enterotoxin; ST motif; tail region; receptor binding region;

KW cytostatic.

XX

OS Escherichia coli.

XX

PH Key Location/Qualifiers

FT Disulfide-bond 6..11

FT Disulfide-bond 7..15

FT Disulfide-bond 10..18

XX

PN WO2003072125-A1.

XX

PD 04-SEP-2003.

XX

PF 21-FEB-2003; 2003WO-US005343.

XX

PR 22-FEB-2002; 2002US-0359204P.

XX

XX AC ADR48359;
XX DT 04-NOV-2004 (first entry)
XX DE Analgesic peptide #2.
XX KW Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
KW neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic;
KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
KW antidabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
KW retinopathy; nephropathy; headache; anxiety; sleep disorder.
XX OS Unidentified.
XX PN WO2004069165-A2.
XX PD 19-AUG-2004.
XX PF 28-JAN-2004; 2004WO-US002390.
XX PR 28-JAN-2003; 2003US-0443098P.
XX PR 15-MAY-2003; 2003US-0471288P.
XX PR 12-NOV-2003; 2003US-0519460P.
XX PA (MICR-) MICROBIA INC.
XX PI Currie MG, Mahajan-Miklos S;
XX WPI; 2004-604332/58.
XX Novel purified peptide capable of activating the guanylate cyclase C
XX receptor, useful for treating obesity, congestive heart failure and
XX benign prostatic hyperplasia.
XX Claim 20; Page 61; 93pp; English.
XX The invention relates to a purified peptide (P1) capable of activating
XX the guanylate cyclase C (GC-C) receptor. Further disclosed is a
XX pharmaceutical composition comprising the peptide of the invention. The
XX composition of the invention is useful for treating a gastrointestinal
XX disorder in a patient, which involves administering P1, where the
XX gastrointestinal disorder is gastrointestinal motility disorder,
XX irritable bowel syndrome, chronic constipation, a functional
XX gastrointestinal disorder, gastroesophageal reflux disease, functional
XX heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
XX gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
XX obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
XX disease. The peptide of the invention is also useful for treating
XX obesity, congestive heart failure, cystic fibrosis or a patient suffering
XX from constipation. The P1/GC-C receptor agonist is useful for treating
XX cancer, respiratory disorder, neurological disorder, disorder associated
XX with carbonate imbalance, erectile dysfunction, insulin-related disorder
XX or inner ear disorder. P1 is useful in treating slow digestion or slow
XX stomach emptying. P1 is useful in relieving symptoms of gastroparesis
XX such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
XX useful for treating or preventing asthma, nephritis, hepatitis, and
XX pancreatitis, allergies, etc. P1 is useful for treating or preventing
XX type II diabetes mellitus, hyperglycaemia, respiratory disorders
XX including inhalation. P1 is useful in treating or preventing retinopathy,
XX nephropathy and edema formation. P1 is useful for treating or preventing
XX headache, anxiety, sleep disorders and memory loss. P1 is useful as a
XX marker to identify, detect, stage, or diagnosis diseases and conditions
XX of the small intestine, including Crohn's disease, colitis, inflammatory
XX bowel disease, tumours, etc. P1 can be conjugated to diagnostic or

CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
CC fibrosis lesions and specific cells lining the intestinal tract, thus
CC useful in targeting radioactive moieties or therapeutic moieties to the
CC intestine to aid in imaging and diagnosing or treating
CC colorectal/metastasised or local colorectal cancer. The current sequence
CC represents an analgesic tag peptide that may form a part of the
CC composition of the invention for the treatment of gastrointestinal
CC disorders.
XX SQ Sequence 19 AA;
Alignment Scores:
Pred. No.: 8,79e-08 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservatives: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 8 Gaps: 0
US-10-775-481A-4 (1-57) x ADR48359 (1-19)
QY 1 AATAGTAGCAATACCTGCTGTAATGTGTTGTAATCTCTGTGAACGGTGCTAT 57
Db 1 AsnSerSerAsnTy:CysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19
RESULT 15
ADR48398
ID ADR48398 standard; peptide; 19 AA.
XX AC ADR48398;
XX DT 04-NOV-2004 (first entry)
XX DE Peptide used in the creation of a wild-type ST peptide.
XX KW Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
KW neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic;
KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
KW antidabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
KW retinopathy; nephropathy; headache; anxiety; sleep disorder.
XX OS Unidentified.
XX PN WO2004069165-A2.
XX PD 19-AUG-2004.
XX PF 28-JAN-2004; 2004WO-US002390.
XX PR 28-JAN-2003; 2003US-0443098P.
XX PR 15-MAY-2003; 2003US-0471288P.
XX PR 12-NOV-2003; 2003US-0519460P.
XX PA (MICR-) MICROBIA INC.
XX PI Currie MG, Mahajan-Miklos S;
XX WPI; 2004-604332/58.
XX Novel purified peptide capable of activating the guanylate cyclase C
XX receptor, useful for treating obesity, congestive heart failure and
XX benign prostatic hyperplasia.
XX Claim 20; Page 61; 93pp; English.
XX The invention relates to a purified peptide (P1) capable of activating
XX the guanylate cyclase C (GC-C) receptor. Further disclosed is a
XX pharmaceutical composition comprising the peptide of the invention. The
XX composition of the invention is useful for treating a gastrointestinal
XX disorder in a patient, which involves administering P1, where the
XX gastrointestinal disorder is gastrointestinal motility disorder,
XX irritable bowel syndrome, chronic constipation, a functional
XX gastrointestinal disorder, gastroesophageal reflux disease, functional
XX heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
XX gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
XX obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
XX disease. The peptide of the invention is also useful for treating
XX obesity, congestive heart failure, cystic fibrosis or a patient suffering
XX from constipation. The P1/GC-C receptor agonist is useful for treating
XX cancer, respiratory disorder, neurological disorder, disorder associated
XX with carbonate imbalance, erectile dysfunction, insulin-related disorder
XX or inner ear disorder. P1 is useful in treating slow digestion or slow
XX stomach emptying. P1 is useful in relieving symptoms of gastroparesis
XX such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
XX useful for treating or preventing asthma, nephritis, hepatitis, and
XX pancreatitis, allergies, etc. P1 is useful for treating or preventing
XX type II diabetes mellitus, hyperglycaemia, respiratory disorders
XX including inhalation. P1 is useful in treating or preventing retinopathy,
XX nephropathy and edema formation. P1 is useful for treating or preventing
XX headache, anxiety, sleep disorders and memory loss. P1 is useful as a
XX marker to identify, detect, stage, or diagnosis diseases and conditions
XX of the small intestine, including Crohn's disease, colitis, inflammatory
XX bowel disease, tumours, etc. P1 can be conjugated to diagnostic or

CC The invention relates to a purified peptide (PI) capable of activating
CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
CC pharmaceutical composition comprising the peptide of the invention. The
CC composition of the invention is useful for treating a gastrointestinal
CC disorder in a patient, which involves administering PI, where the
CC gastrointestinal disorder is gastrointestinal motility disorder,
CC irritable bowel syndrome, chronic constipation, a functional
CC gastrointestinal disorder, gastroesophageal reflux disease, functional
CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
CC disease. The peptide of the invention is also useful for treating
CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
CC from constipation. The PI/GC-C receptor agonist is useful for treating
CC cancer, respiratory disorder, neurological disorder, disorder associated
CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
CC or inner ear disorder. PI is useful in treating slow digestion or slow
CC stomach emptying. PI is useful in relieving symptoms of gastroparesis,
CC such as nausea, vomiting, bloating, and delayed gastric emptying. PI is
CC useful for treating or preventing asthma, nephritis, hepatitis,
CC pancreatitis, allergies, etc. PI is useful for treating or preventing
CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
CC including inhalation. PI is useful in treating or preventing retinopathy,
CC nephropathy and edema formation. PI is useful for treating or preventing
CC headache, anxiety, sleep disorders and memory loss. PI is useful as a
CC marker to identify, detect, stage, or diagnosis diseases and conditions
CC of the small intestine, including Crohn's disease, colitis, inflammatory
CC bowel disease, tumours, etc. PI can be conjugated to diagnostic or
CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
CC fibrosis lesions and specific cells lining the intestinal tract, thus
CC useful in targeting radioactive moieties or therapeutic moieties to the
CC intestine to aid in imaging and diagnosing or treating
CC colorectal/metastasised or local colorectal cancer. The current sequence
CC represents an peptide used in an example from the invention in the
CC preparation of variant ST peptides and wild-type ST peptide.

XX
SQ Sequence 19 AA;

Alignment Scores:

Pred. No.:	8.79e-08	Length:	19
Score:	120.00	Matches:	18
Percent Similarity:	94.74%	Conservative:	0
Best Local Similarity:	94.74%	Mismatches:	1
Query Match:	95.24%	Indels:	0
DB:	8	Gaps:	0

US-10-775-481A-4 (1-57) x ADR48398 (1-19)

Qy	1	AATAGTACCAATTACTGCTGTGAATTGTTGTGTAATCCTGCTTGTACGGGTGCTAT	57
Db	1	AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr	19

Search completed: March 26, 2005, 17:47:43
Job time : 90.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 26, 2005, 17:41:22 ; Search time 30 Seconds
(without alignments)
283.666 Million cell updates/sec

Title: US-10-775-481A-4

Perfect score: 126

Sequence: 1 aatagtagcaattactgtg.....ctgttgtaacgggtgtat 57

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued_Patents_AA -QPMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DSELP=6 -DELEXT=7

Database :

Issued Patents AA:
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pcp:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	19	1	US-08-141-892A-5
2	126	100.0	19	2	US-08-583-447A-5
3	126	100.0	19	3	US-08-467-920-5
4	126	100.0	19	3	US-08-635-930-5
5	126	100.0	19	3	US-09-193-997-5
6	126	100.0	19	3	US-09-138-237A-5
7	114	90.5	18	1	US-08-141-892A-33
8	114	90.5	18	2	US-08-583-447A-33
9	114	90.5	18	2	US-08-467-920-33
10	114	90.5	18	3	US-08-635-930-33
11	114	90.5	18	3	US-09-193-997-33
12	114	90.5	18	3	US-09-138-237A-33

13	113	89.7	18	1	US-08-141-892A-27
14	113	89.7	18	2	US-08-583-447A-27
15	113	89.7	18	2	US-08-467-920-27
16	113	89.7	18	3	US-08-635-930-27
17	113	89.7	18	3	US-09-193-997-27
18	113	89.7	18	3	US-09-138-237A-27
19	112	88.9	19	1	US-08-141-892A-49
20	112	88.9	19	2	US-08-583-447A-49
21	112	88.9	19	2	US-08-467-920-49
22	112	88.9	19	3	US-08-635-930-49
23	112	88.9	19	3	US-09-193-997-49
24	112	88.9	19	3	US-09-138-237A-49
25	110	87.3	17	1	US-08-141-892A-34
26	110	87.3	17	2	US-08-583-447A-34
27	110	87.3	17	2	US-08-467-920-34
28	110	87.3	17	3	US-08-635-930-34
29	110	87.3	17	3	US-09-193-997-34
30	110	87.3	17	3	US-09-138-237A-34
31	107	84.9	17	1	US-08-141-892A-28
32	107	84.9	17	2	US-08-583-447A-28
33	107	84.9	17	2	US-08-467-920-28
34	107	84.9	17	3	US-08-635-930-28
35	107	84.9	17	3	US-09-193-997-28
36	107	84.9	17	3	US-09-138-237A-28
37	106	84.1	16	1	US-08-141-892A-35
38	106	84.1	16	2	US-08-583-447A-35
39	106	84.1	16	2	US-08-467-920-35
40	106	84.1	16	3	US-08-635-930-35
41	106	84.1	16	3	US-09-193-997-35
42	106	84.1	16	3	US-09-138-237A-35
43	103	81.7	16	1	US-08-141-892A-29
44	103	81.7	16	2	US-08-583-447A-29
45	103	81.7	16	2	US-08-467-920-29

ALIGNMENTS

RESULT 1

US-08-141-892A-5

Sequence 5, Application US/08141892A

Patent No. 5518888

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and Methods

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/141,892A

FILING DATE: 26-OCT-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-0903

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-141-892A-5

Alignment Scores:
Pred. No.: 4.67e-10 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-141-892A-5 (1-19)

QY 1 AATAGTAGCAATTAAGTCTGTGAATGTTGTGTAATCCTGTTGTAACGGGTGCTAT 57
DB 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 2

US-08-583-447A-5
Sequence 5, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using The Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-447A-5

Alignment Scores:
Pred. No.: 4.67e-10 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-583-447A-5 (1-19)

QY 1 AATAGTAGCAATTAAGTCTGTGAATGTTGTGTAATCCTGTTGTAACGGGTGCTAT 57
DB 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 3

US-08-467-920-5
Sequence 5, Application US/08467920
Patent No. 5962220
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5962220ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-920-5

Alignment Scores:
Pred. No.: 4.67e-10 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-467-920-5 (1-19)

QY 1 AATAGTAGCAATTAAGTCTGTGAATGTTGTGTAATCCTGTTGTAACGGGTGCTAT 57
DB 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 4

US-08-635-930-5
Sequence 5, Application US/08635930
Patent No. 6060037
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically Bind To

;; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
;; TITLE OF INVENTION: The Same
;; NUMBER OF SEQUENCES: 54
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
;; STREET: One Liberty Place, 46th Floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: WINDOWS 3.1
;; SOFTWARE: WordPerfect 6.0/6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/635,930
;; FILING DATE: 26-APR-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/141,892
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/305,056
;; FILING DATE: 13-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeLuca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1360
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-635-930-5

Alignment Scores:
Pred. No.: 4.67e-10 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-635-930-5 (1-19)
Qy 1 AATAGTAGCAATTCCTGCTGTAATCTGTTGTAATCTGCTTCTAAGCGGTGCTAT 57
Db 1 AasSerSerAenTyCyCysGluLeuCysCysAsnProAlaCysAsnGlyCysTy 19

RESULT 5
US-09-193-997-5
; Sequence 5, Application US/09193997
; Patent No. 6087109
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6087109ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA

;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/193,997
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/467,920
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeLuca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1589
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-193-997-5

Alignment Scores:
Pred. No.: 4.67e-10 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-775-481A-4 (1-57) x US-09-193-997-5 (1-19)
Qy 1 AATAGTAGCAATTCCTGCTGTAATCTGTTGTAATCTGCTTCTAAGCGGTGCTAT 57
Db 1 AasSerSerAenTyCyCysGluLeuCysCysAsnProAlaCysAsnGlyCysTy 19

RESULT 6
US-09-138-237A-5
; Sequence 5, Application US/09138237A
; Patent No. 6268159
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch disk, 720 Kb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/138,237A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/141,892
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-138-237A-5

Alignment Scores:
Pred. No.: 4.67e-10 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-775-481A-4 (1-57) x US-09-138-237A-5 (1-19)

QY 1 AATAGCAATTAAGTCTGCTGTAATGTTGTAATCTCTGTTGAACGGGTGCTAT 57
Db 1 AsnSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 7

US-08-141-892A-33
Sequence 33, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,892A
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-141-892A-33

Alignment Scores:
Pred. No.: 2.33e-08 Length: 18
Score: 114.00 Matches: 17

Percent Similarity: 94.44% Conservative: 0
Best Local Similarity: 94.44% Mismatches: 1
Query Match: 90.48% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-141-892A-33 (1-18)

QY 4 AATAGCAATTAAGTCTGCTGTAATGTTGTAATCTCTGTTGAACGGGTGCTAT 57
Db 1 SerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 18

RESULT 8

US-08-583-447A-33
Sequence 33, Application US/08583447A
Patent No. 5879656
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
TITLE OF INVENTION: Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-583-447A-33

Alignment Scores:
Pred. No.: 2.33e-08 Length: 18
Score: 114.00 Matches: 17
Percent Similarity: 94.44% Conservative: 0
Best Local Similarity: 94.44% Mismatches: 1
Query Match: 90.48% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-583-447A-33 (1-18)

QY 4 AATAGCAATTAAGTCTGCTGTAATGTTGTAATCTCTGTTGAACGGGTGCTAT 57
Db 1 SerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 18

RESULT 9

US-08-467-920-33
Sequence 33, Application US/08467920
Patent No. 5962220

GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5962220ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,920
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-920-33

Alignment Scores:
Pred. No.: 2,33e-08 Length: 18
Score: 114.00 Matches: 17
Percent Similarity: 94.44% Conservatives: 0
Best Local Similarity: 94.44% Mismatches: 1
Query Match: 90.48% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-467-920-33 (1-18)

Qy 4 AGTAGCAATTACTGCTGTGAATTGTTGTGAATCTGCTGTACGGGTGCTAT 57
Db 1 SerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 18

RESULT 10
US-08-635-930-33
Sequence 33, Application US/08635930
Patent No. 6060037
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically Bind To
TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
TITLE OF INVENTION: The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 3.1
SOFTWARE: WordPerfect 6.0/6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,930
FILING DATE: 26-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-635-930-33

Alignment Scores:
Pred. No.: 2,33e-08 Length: 18
Score: 114.00 Matches: 17
Percent Similarity: 94.44% Conservatives: 0
Best Local Similarity: 94.44% Mismatches: 1
Query Match: 90.48% Indels: 0
DB: 3 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-635-930-33 (1-18)

Qy 4 AGTAGCAATTACTGCTGTGAATTGTTGTGAATCTGCTGTACGGGTGCTAT 57
Db 1 SerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 18

RESULT 11
US-09-193-997-33
Sequence 33, Application US/09193997
Patent No. 6087109
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 6087109ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
FILING DATE:
CLASSIFICATION:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,920
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-193-997-33

Alignment Scores:
Pred. No.: 2.33e-08 Length: 18
Score: 114.00 Matches: 17
Percent Similarity: 94.44% Conservative: 0
Best Local Similarity: 94.44% Mismatches: 1
Query Match: 90.48% Indels: 0
DB: 3 Gaps: 0

US-10-775-481A-4 (1-57) x US-09-193-997-33 (1-18)

QY 4 AGTAGCAATTACTGCTGTAATGTGTGTAATCTGCTGTGTAACGGGTGCTAT 57
Db 1 SerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 18

RESULT 12
US-09-138-237A-33
; Sequence 33, Application US/09138237A
; Patent No. 6268159
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,237A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-138-237A-33

Alignment Scores:
Pred. No.: 3.22e-08 Length: 18
Score: 113.00 Matches: 17
Percent Similarity: 94.44% Conservative: 0
Best Local Similarity: 94.44% Mismatches: 1
Query Match: 89.68% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x US-09-138-237A-33 (1-18)

QY 4 AGTAGCAATTACTGCTGTAATGTGTGTAATCTGCTGTGTAACGGGTGCTAT 57
Db 1 SerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 18

RESULT 13
US-08-141-892A-27
; Sequence 27, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-141-892A-27

Alignment Scores:
Pred. No.: 3.22e-08 Length: 18
Score: 113.00 Matches: 17
Percent Similarity: 94.44% Conservative: 0
Best Local Similarity: 94.44% Mismatches: 1
Query Match: 89.68% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-141-892A-27 (1-18)

QY 1 AATAGTAGCAATTACTGCTGTAATGTGTGTAATCTGCTGTGTAACGGGTGCTAT 54
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCys 18
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RESULT 14

US-08-583-447A-27
; Sequence 27, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583.447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141.892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-583-447A-27

Alignment Scores:

Pred. No.:	3.22e-08	Length:	18
Score:	113.00	Matches:	17
Percent Similarity:	94.44%	Conservative:	0
Best Local Similarity:	94.44%	Mismatches:	1
Query Match:	89.68%	Indels:	0
DB:	2	Gaps:	0

US-10-775-481A-4 (1-57) x US-08-583-447A-27 (1-18)

Qy 1 AATAGTAGCAATTACTGTGTAATTGTTGTAATCTGCTGTAAACGGGTGC 54
|||||
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCys 18
|||||

RESULT 15

US-08-467-920-27
; Sequence 27, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSSEE: NO. 5962220ris
; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-467-920-27

Alignment Scores:
Pred. No.: 3.22e-08 Length: 18
Score: 113.00 Matches: 17
Percent Similarity: 94.44% Conservative: 0
Best Local Similarity: 94.44% Mismatches: 1
Query Match: 89.68% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-467-920-27 (1-18)

Qy 1 AATAGTAGCAATTACTGTGTAATTGTTGTAATCTGCTGTAAACGGGTGC 54
|||||
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCys 18
|||||

Search completed: March 26, 2005, 17:52:56
Job time : 31 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 26, 2005, 17:50:53 ; Search time 68 Seconds

(without alignments)
555.081 Million cell updates/sec

Title: US-10-775-481A-4

Perfect score: 126

Sequence: 1 aatagtagcaattactctgctg.....ctgctgttaacgggtgctat 57

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 2814804

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPRO_spool_p/US10775481/runat_25032005_151020_7906/app_query.fasta_1.199
-DB=Published Applications_AA -QFMT=fastan -ENDF=1 -MATRIX=blseum62
-TRANSPCU=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blseum62
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -THR SCORE=ptc -THR MAX=100
-MAXLEN=2000000000 -PGR=US10775481 @CGN 1.130 @runat_25032005_151020_7906
-NCPU=6 -ICPU=3 -NO MWAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	126	100.0	19	15	US-10-621-684-5	Sequence 5, Appli
2	120	95.2	19	14	US-10-107-814-23	Sequence 23, Appli
3	120	95.2	19	15	US-10-371-966-1	Sequence 1, Appli
4	120	95.2	19	17	US-10-796-719-1	Sequence 26, Appli
5	120	95.2	19	17	US-10-796-719-26	Sequence 7, Appli
6	120	95.2	21	17	US-10-479-606-7	Sequence 39, Appli
7	120	95.2	21	17	US-10-796-719-39	Sequence 21, Appli
8	120	95.2	72	17	US-10-796-719-21	Sequence 84, Appli
9	118	93.7	19	17	US-10-796-719-84	Sequence 86, Appli
10	118	93.7	19	17	US-10-796-719-86	Sequence 92, Appli
11	117	92.9	19	15	US-10-796-719-92	Sequence 2, Appli
12	116	92.1	19	17	US-10-371-966-2	Sequence 27, Appli
13	116	92.1	19	17	US-10-796-719-27	Sequence 87, Appli
14	116	92.1	21	17	US-10-796-719-40	Sequence 40, Appli
15	116	92.1	21	17	US-10-796-719-41	Sequence 41, Appli
16	116	92.1	19	17	US-10-796-719-28	Sequence 28, Appli
17	115	91.3	19	17	US-10-796-719-75	Sequence 75, Appli
18	115	91.3	19	17	US-10-796-719-79	Sequence 79, Appli
19	115	91.3	19	17	US-10-796-719-90	Sequence 90, Appli
20	115	91.3	21	17	US-10-796-719-42	Sequence 42, Appli
21	115	91.3	18	15	US-10-621-684-33	Sequence 33, Appli
22	114	90.5	19	17	US-10-796-719-76	Sequence 76, Appli
23	114	90.5	19	17	US-10-796-719-80	Sequence 80, Appli
24	114	90.5	19	17	US-10-796-719-85	Sequence 85, Appli
25	114	90.5	19	17	US-10-796-719-89	Sequence 89, Appli
26	114	90.5	19	17	US-10-796-719-91	Sequence 91, Appli
27	114	90.5	21	17	US-10-796-719-43	Sequence 43, Appli
28	114	90.5	21	17	US-10-796-719-44	Sequence 44, Appli
29	114	90.5	21	17	US-10-796-719-45	Sequence 45, Appli
30	113	89.7	18	15	US-10-621-684-27	Sequence 27, Appli
31	113	89.7	19	17	US-10-796-719-77	Sequence 77, Appli
32	113	89.7	19	17	US-10-796-719-81	Sequence 81, Appli
33	113	89.7	19	17	US-10-796-719-88	Sequence 88, Appli
34	113	89.7	19	17	US-10-796-719-88	Sequence 88, Appli
35	112	88.9	19	15	US-10-621-684-49	Sequence 49, Appli
36	112	88.9	19	17	US-10-796-719-68	Sequence 68, Appli
37	112	88.9	19	17	US-10-796-719-78	Sequence 78, Appli
38	112	88.9	19	17	US-10-796-719-82	Sequence 82, Appli
39	112	88.9	17	15	US-10-621-684-34	Sequence 34, Appli
40	110	86.5	18	17	US-10-796-719-72	Sequence 72, Appli
41	109	86.5	19	17	US-10-796-719-69	Sequence 69, Appli
42	109	86.5	19	17	US-10-796-719-70	Sequence 70, Appli
43	109	86.5	19	17	US-10-796-719-71	Sequence 71, Appli
44	109	86.5	19	17	US-10-796-719-71	Sequence 71, Appli
45	109	86.5	19	17	US-10-796-719-71	Sequence 71, Appli

ALIGNMENTS

RESULT 1
US-10-621-684-5
Sequence 5, Application US/10621684
Publication No. US20040029182A1
GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and

Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1r18

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-621-684-5

Alignment Scores:
Pred. No.: 2,06e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-621-684-5 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTGAATTGTGTGTAATCCTGCTTGTAAACGGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 2

US-10-775-481A-4 (1-57) x US-10-621-684-5 (1-19)
; Sequence 23, Application US/10/07814
; Publication No. US20030073628A1
; GENERAL INFORMATION:
; APPLICANT: SHAILUBHAI, KUNWAR
; APPLICANT: JACOB, GARY S.
; APPLICANT: NIKIFOROVICH, GREGORY
; TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
; OF TISSUE INFLAMMATION AND CARCINOGENESIS
; FILE REFERENCE: 81361/284943/WAS
; CURRENT APPLICATION NUMBER: US/10/107,814
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (6)..(10)
; NAME/KEY: DISULFID
; LOCATION: (7)..(15)
; NAME/KEY: DISULFID
; LOCATION: (11)..(18)
US-10-107-814-23

Alignment Scores:
Pred. No.: 1.3e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 14 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-107-814-23 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTGAATTGTGTGTAATCCTGCTTGTAAACGGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 3

US-10-371-966-1
; Sequence 1, Application US/10371966
; Publication No. US20030232013A1
; GENERAL INFORMATION:
; APPLICANT: SIECKMAN, GARY
; APPLICANT: VOLKERT, WYNN
; APPLICANT: FORTE, LEONARD
; APPLICANT: HOFFMAN, TIMOTHY
; APPLICANT: GALI, HARIPRASAD
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TARGETING OF CANCERS CELLS
; WITH TUMOR HOMING PEPTIDES
; FILE REFERENCE: UVM0:013US
; CURRENT APPLICATION NUMBER: US/10/371,966
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/359,204
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-371-966-1

Alignment Scores:

Pred. No.: 1.3e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 15 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-371-966-1 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTGAATTGTGTGTAATCCTGCTTGTAAACGGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 4

US-10-796-719-1
; Sequence 1, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19

; CURRENT APPLICATION NUMBER: US/10/479,606

; Sequence 21, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-21

Alignment Scores:
Pred. No.: 1.16e-07 Length: 72
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservatives: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 17 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-796-719-21 (1-72)

OY 1 AATAGTAGCAATTACTGCTGTGAATGTGTGTAATCTGCTTGTAAACGGGTGCTAT 57
|||||
Db 54 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72
|||||

RESULT 9

US-10-796-719-84
; Sequence 84, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-84

Alignment Scores:
Pred. No.: 2.4e-07 Length: 19
Score: 118.00 Matches: 17

Percent Similarity: 94.74% Conservatives: 1
Best Local Similarity: 89.47% Mismatches: 1
Query Match: 93.65% Indels: 0
DB: 17 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-796-719-84 (1-19)

OY 1 AATAGTAGCAATTACTGCTGTGAATGTGTGTAATCTGCTTGTAAACGGGTGCTAT 57
|||||
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19
|||||

RESULT 10

US-10-796-719-86
; Sequence 86, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-86

Alignment Scores:
Pred. No.: 2.4e-07 Length: 19
Score: 118.00 Matches: 17
Percent Similarity: 94.74% Conservatives: 1
Best Local Similarity: 89.47% Mismatches: 1
Query Match: 93.65% Indels: 0
DB: 17 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-796-719-86 (1-19)

OY 1 AATAGTAGCAATTACTGCTGTGAATGTGTGTAATCTGCTTGTAAACGGGTGCTAT 57
|||||
Db 1 AsnSerSerAsnTyrCysCysGluMetCysCysAsnProAlaCysThrGlyCysTyr 19
|||||

RESULT 11

US-10-796-719-92
; Sequence 92, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15

; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-92

Alignment Scores:
Pred. No.: 3.27e-07 Length: 19
Score: 117.00 Matches: 17
Percent Similarity: 94.74% Conservativeness: 1
Best Local Similarity: 89.47% Mismatches: 1
Query Match: 92.86% Indels: 0
DB: 17 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-796-719-92 (1-19)

Qy 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTAATCTGCTTGTAAAGGGTGCTAT 57
Db 1 AsnSerSerAenTyrcysCysGluValCysCysAsnProAlaCysThrGlyCysPhe 19

RESULT 12

US-10-371-966-2

; Sequence 2, Application US/10371966
; Publication No. US20030232013A1
; GENERAL INFORMATION:
; APPLICANT: SIECKMAN, GARY
; APPLICANT: VOLKERT, WYNN
; APPLICANT: FORTE, LEONARD
; APPLICANT: HOFFMAN, TIMOTHY
; APPLICANT: GALLI, HARIPRASAD
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TARGETING OF CANCERS CELLS
; FILE OF INVENTION: WITH TUMOR HOMING PEPTIDES
; FILE REFERENCE: UYMO:013US
; CURRENT APPLICATION NUMBER: US/10/371,966
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/359,204
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-371-966-2

Alignment Scores:
Pred. No.: 4.44e-07 Length: 19
Score: 116.00 Matches: 17
Percent Similarity: 94.74% Conservativeness: 1
Best Local Similarity: 89.47% Mismatches: 1
Query Match: 92.06% Indels: 0
DB: 15 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-371-966-2 (1-19)

Qy 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTAATCTGCTTGTAAAGGGTGCTAT 57
Db 1 AsnSerSerAenTyrcysCysGluLeuCysCysAsnProAlaCysThrGlyCysPhe 19

RESULT 13

US-10-796-719-27

; Sequence 27, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:

; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-27

Alignment Scores:
Pred. No.: 4.44e-07 Length: 19
Score: 116.00 Matches: 18
Percent Similarity: 94.74% Conservativeness: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 92.06% Indels: 0
DB: 17 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-796-719-27 (1-19)

Qy 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTAATCTGCTTGTAAAGGGTGCTAT 57
Db 1 AsnSerSerAenTyrcysCysGluLeuCysCysAsnProAlaCysThrGlyCysPhe 19

RESULT 14

US-10-796-719-87
; Sequence 87, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-87

Alignment Scores:
Pred. No.: 4.44e-07 Length: 19
Score: 116.00 Matches: 17
Percent Similarity: 89.47% Conservativeness: 0

Job time : 69 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 26, 2005, 17:40:12 ; Search time 25 Seconds
(without alignments)
438.748 Million cell updates/sec

Title: US-10-775-481A-4
Perfect score: 126
Sequence: 1 aatagtagcaattactgctg.....ctgcttgtaacgggtgctat 57

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO_spool_P/US10775481/runat_25032005_151018_7801/app_query.fasta_1.199
-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10775481 @CGN 1.1.38 @runat_25032005_151018_7801 -NCPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	95.2	72	1 QHEC4	heat-stable entero
2	120	95.2	72	1 QHEC1B	heat-stable entero
3	103	81.7	72	1 QHEC1	heat-stable entero
4	98	77.8	18	2 A60103	heat-stable entero
5	89	70.6	53	2 S68705	heat-stable entero
6	88	69.8	66	2 S31652	enterotoxin - Yers
7	88	65.9	18	1 QHEC2	heat-stable entero
8	81	64.3	17	2 A34534	heat-stable entero
9	81	64.3	78	1 QHVC1	heat-stable entero
10	78.5	62.3	71	2 S25659	heat-stable entero
11	69	54.8	65	2 S34671	heat-stable entero
12	62.5	49.6	186	2 A45910	ultra-high-sulfur
13	59	46.8	112	2 JC4651	uroguanylin precu
14	58	46.0	116	2 JC7620	guanylin precursor

15	54.5	43.3	122	2	JC6548	high sulfur protei
16	54.5	43.3	369	2	T24022	hypothetical prote
17	54	42.9	56	1	WTFP	testis-specific pr
18	54	42.9	68	2	S25775	testis-specific pr
19	54	42.9	415	2	T19234	hypothetical prote
20	53.5	42.5	64	2	A25775	metallothionein A
21	53.5	42.5	64	2	A33825	metallothionein A
22	53.5	42.5	410	2	T24020	hypothetical prote
23	53	42.1	173	2	T37284	cysteine proteinas
24	53	42.1	172	2	T47106	high-sulfur wool m
25	53	42.1	400	2	T22853	probable cathepsin
26	53	51.0	423	2	TS0923	acetylornithine tr
27	52.5	41.7	152	2	T18975	hypothetical prote
28	52.5	41.7	164	2	T24272	hypothetical prote
29	52.5	41.7	176	2	T31796	hypothetical prote
30	52.5	41.7	188	2	T15651	hypothetical prote
31	52	41.3	152	1	KRSHHC	keratin high-sulfu
32	52	41.3	152	2	I47111	high-sulfur wool m
33	52	41.3	152	2	I47109	high-sulfur wool m
34	52	41.3	152	2	I47108	high-sulfur wool m
35	52	41.3	152	2	I47112	high-sulfur wool m
36	52	41.3	156	1	KRSHHB	keratin high-sulfu
37	52	41.3	162	2	I47107	high-sulfur wool m
38	52	41.3	172	1	KRSHHA	keratin high-sulfu
39	52	41.3	182	1	KRSHHD	keratin high-sulfu
40	52	41.3	182	2	I47105	high-sulfur wool m
41	52	41.3	188	2	JC6547	high sulfur protei
42	52	41.3	1299	2	T43251	furin (EC 3.4.21.7
43	51	40.5	248	2	T19913	hypothetical prote
44	51	40.5	525	2	G71317	hypothetical prote
45	51	40.5	810	1	A33380	interleukin-4 rece

ALIGNMENTS

RESULT 1

QHEC4

heat-stable enterotoxin STA4 precursor - Escherichia coli

C:Species: Escherichia coli

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: J070373; A35978

R:Stegeltz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Bolivar, F.;

Plasmid 20, 42-53, 1988

A>Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri

A:Reference number: J070373; PMID:89202548; PMID:3071819

A:Accession: J070373

A:Molecule type: DNA

A:Residues: 1-72 <STI>

R:Zhou, X.; Shen, L.P.; Chi, C.W.

Toxicol 28, 453-456, 1990

A>Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stabl

A:Reference number: A35978; PMID:90273381; PMID:2190361

A:Accession: A35978

A:Molecule type: DNA

A:Residues: 1-72 <ZHO>

C:Genetics:

A:Gene: estA4

C:Superfamily: heat-stable enterotoxin ST

C:Keywords: enterotoxin; heat-stable protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-53/Domain: propeptide #status predicted <PRO>

F:54-72/Product: heat-stable enterotoxin #status predicted <MAT>

F:59-64,60-68,63-71/disulfide bonds: #status predicted

Alignment Scores:

Pred. No.:	5.03e-09	Length:	72
Score:	120.00	Matches:	18
Percent Similarity:	94.74%	Conservative:	0
Best Local Similarity:	94.74%	Mismatches:	1
Query Match:	95.24%	Indels:	0
DB:	1	Gaps:	0

US-10-775-481A-4 (1-57) x QHEC4 (1-72)

QY 1 AATAGTACCAATTACTGCTGTAATGTTGTTGTAATCTGCTTGTAAACGGGTGCTAT 57

Db 54 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

RESULT 2

QHECIB

heat-stable enterotoxin ST-Ib precursor - Escherichia coli

N:Alternate names: heat-stable enterotoxin ST-A2

C:Species: Escherichia coli

C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004

C:Accession: J030292; A33068; A33067; A30567

R:Moseley, S.L.; Hardy, J.W.; Huq, M.I.; Echeverria, P.; Falkow, S.

Infect. Immun. 39, 1167-1174, 1983

A:Title: Isolation and nucleotide determination of a gene encoding a heat-stable enterotoxin

A:Reference number: J030292; MUID:83184648; PMID:6341230

A:Accession: J030292

A:Molecule type: DNA

A:Residues: 1-72 <MOS>

A:Cross-references: UNIPROT:O47185; UNIPROT:P07965; GB:M34916; NID:G146407; PIDN:AAA2399

R:Dwarakanath, P.; Visweswariah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha, Gene 81, 219-226, 1989

A:Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of Escherichia coli

A:Reference number: A33068; MUID:90034194; PMID:2680769

A:Accession: A33068

A:Molecule type: DNA

A:Residues: 1-18, 'A', 20-72 <DNA>

A:Cross-references: GB:M29255; NID:G148029; PIDN:AAA24686.1; PID:G148030

A>Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34

R:Almoco, S.; Takao, T.; Shimomishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T.

Eur. J. Biochem. 129, 257-263, 1982

A:Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic Escherichia coli

A:Reference number: A33067; MUID:83105138; PMID:6759126

A:Accession: A33067

A:Molecule type: protein

A:Residues: 54-72 <AIM>

R:Guzman-Verduzco, L.M.; Kupersztosch, Y.M.

Infect. Immun. 57, 645-648, 1989

A:Title: Rectification of two Escherichia coli heat-stable enterotoxin allele sequences

A:Reference number: A30567; MUID:89108616; PMID:2643580

A:Accession: A30567

A:Molecule type: DNA

A:Residues: 1-18, 'A', 20-24, 'AG', 27-41, 'V', 43-44, 'N', 46, 'E', 48, 'S', 50-72 <GUZ>

A:Cross-references: GB:M18345; NID:G145862; PIDN:AAA23729.1; PID:G145863

C:Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.

C:Genetics:

A:Gene: st

C:Superfamily: heat-stable enterotoxin ST

C:Keywords: enterotoxin; heat-stable protein

F:1-53/Domain: signal sequence and propeptide

F:54-72/Product: heat-stable enterotoxin ST-Ib #status experimental <MAT>

F:59-64,60-68,63-71/Disulfide bonds: #status experimental

Alignment Scores:

Pred. No.: 5.03e-09 Length: 72

Score: 120.00 Matches: 18

Percent Similarity: 94.74% Conservative: 0

Best Local Similarity: 94.74% Mismatches: 1

Query Match: 95.24% Indels: 0

DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x QHECIB (1-72)

QY 1 AATAGTACCAATTACTGCTGTAATGTTGTTGTAATCTGCTTGTAAACGGGTGCTAT 57

Db 54 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

RESULT 3

QHEC1

heat-stable enterotoxin ST-I precursor - Escherichia coli

N:Alternate names: heat-stable enterotoxin estal

C:Species: Escherichia coli

QY 1 AATAGTACCAATTACTGCTGTAATGTTGTTGTAATCTGCTTGTAAACGGGTGCTAT 57

Db 54 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

RESULT 4

QHEC1

heat-stable enterotoxin ST-Ia - Citrobacter freundii

C:Species: Citrobacter freundii

C>Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

R:Guarino, A.; Giannella, R.; Thompson, M.R.

C>Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 09-Jul-2004

C:Accession: A01822; A30985; A36732; JT0374; I51932

R:SO, M.; McCarthy, B.J.

Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980

A:Title: Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stable enterotoxin

A:Reference number: A01822; MUID:81054703; PMID:6254008

A:Accession: A01822

A:Molecule type: DNA

A:Residues: 1-72 <LAZ>

A:Cross-references: UNIPROT:P01559; GB:V00612; GB:J01831; NID:G43704; PIDN:CAA23883.1; PID:G43704

R:Lazure, C.; Seidab, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S.

Can. J. Biochem. Cell Biol. 61, 287-292, 1983

A:Title: Primary structure determination of Escherichia coli heat-stable enterotoxin of 18D

A:Reference number: A30985; MUID:83284515; PMID:6349752

A:Accession: A30985

A:Molecule type: protein

A:Residues: 55-72 <LAZ2>

A:Experimental source: strain F11

R:Dallas, W.S.

J. Bacteriol. 172, 5490-5493, 1990

A:Title: The heat-stable toxin I gene from Escherichia coli 18D.

A:Reference number: A36732; MUID:90368614; PMID:2203756

A:Accession: A36732

A:Molecule type: DNA

A:Residues: 1-72 <DAL>

A:Cross-references: GB:M58746; NID:G145860; PIDN:AAA62776.1; PID:G145861

A:Experimental source: strain 18D

R:Stiegitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Plasmid 20, 42-53, 1988

A:Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escherichia coli heat-stable enterotoxin gene

A:Reference number: JT0373; MUID:89202548; PMID:3071819

A:Accession: JT0373

A:Molecule type: DNA

A:Residues: 1-72 <STI>

A:Experimental source: strain 18D

R:Sekizaki, T.; Akashi, H.; Terakado, N.

Am. J. Vet. Res. 46, 909-912, 1985

A:Title: Nucleotide sequences of the genes for Escherichia coli heat-stable enterotoxin I and II

A:Reference number: I51932; MUID:85249571; PMID:2990268

A:Accession: I51932

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-69, 'P', 71-72 <RES>

A:Cross-references: GB:M25607; NID:G147877; PIDN:AAA24653.1; PID:G147878

C:Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic strains of Escherichia coli.

C:Superfamily: heat-stable enterotoxin ST

C:Keywords: enterotoxin; heat-stable protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-54/Domain: propeptide #status predicted <PRO>

F:55-72/Product: heat-stable enterotoxin ST-I #status experimental <MAT>

F:59-64,60-68,63-71/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.: 1.33e-06 Length: 72

Score: 103.00 Matches: 15

Percent Similarity: 89.47% Conservative: 2

Best Local Similarity: 78.95% Mismatches: 2

Query Match: 81.75% Indels: 0

DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x QHEC1 (1-72)

QY 1 AATAGTACCAATTACTGCTGTAATGTTGTTGTAATCTGCTTGTAAACGGGTGCTAT 57

Db 54 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

RESULT 4

A60103

heat-stable enterotoxin ST-Ia - Citrobacter freundii

C:Species: Citrobacter freundii

C>Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

R:Guarino, A.; Giannella, R.; Thompson, M.R.

Infect. Immun. 57, 649-652, 1989
A:Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identical to enterotoxin of *Escherichia coli* serotype O157
A:Reference number: A60103; MUID:89108617; PMID:2912902
A:Accession: A60103
A:Molecule type: protein
A:Residues: 1-18 <GUA>
A:Cross-references: UNIPROT:O7M0U3
C:Superfamily: heat-stable enterotoxin ST

Alignment Scores:
Pred. No.: 1e-05 Length: 18
Score: 98.00 Matches: 14
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 1
Query Match: 77.78% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x A60103 (1-18)

Qy 13 TACTGCTGTGAATGTGTGTAATCTCTGTGTAACGGGTCTAT 57
|||||
Db 4 TyrCysGluLeuCysCysAsnProAlaCysAlaGlyCysTyr 18
|||||

RESULT 5
S68705
heat-stable enterotoxin Y-Stc - Yersinia enterocolitica
C:Species: Yersinia enterocolitica
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: S68705
R:Yoshino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimonishi, Y.
FEMS Lett. 362, 319-322, 1995
A:Title: Characterization of a highly toxic, large molecular size heat-stable enterotoxin of *Yersinia enterocolitica* serotype O3
A:Reference number: S68705; MUID:95246844; PMID:7729521
A:Accession: S68705
A:Molecule type: protein
A:Residues: 1-53 <YOS>
A:Experimental source: strain 86-11
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:41-46,42-50,45-53/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 0.000143 Length: 53
Score: 89.00 Matches: 13
Percent Similarity: 83.33% Conservative: 2
Best Local Similarity: 72.22% Mismatches: 3
Query Match: 70.63% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x S68705 (1-53)

Qy 1 AATAGTAGCAATTACTGCTGTGAATGTGTGTAATCTCTGTGTAACGGGTGC 54
|||||
Db 36 AsnAspTrpAspTrpCysCysGluLeuCysCysAsnProAlaCysPheGlyCys 53
|||||

RESULT 6
S31652
enterotoxin - Yersinia kristensenii
C:Species: Yersinia kristensenii
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S31652
R:Ibrahim, A.; Liesack, W.; Stackebrandt, E.
submitted to the EMBL Data Library, November 1992
A:Reference number: S31652
A:Accession: S31652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-66 <IBR>
A:Cross-references: UNIPROT:P31518; EMBL:X69218; NID:G48617; PIDN:CAA49152.1; PID:G48618
C:Superfamily: heat-stable enterotoxin ST

Alignment Scores:
Pred. No.: 0.000187 Length: 66

Score: 88.00 Matches: 12
Percent Similarity: 93.75% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 69.84% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x S31652 (1-66)

Qy 7 AGCAATTACTCTGTGAATGTGTGTAATCTCTGTGTAACGGGTGC 54
|||||
Db 51 SerAspTrpCysCysGluValCysCysAsnProAlaCysAlaGlyCys 66
|||||

RESULT 7
QHEC2
heat-stable enterotoxin ST-2 - Escherichia coli
C:Species: Escherichia coli
C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
C:Accession: A01823
R:Chan, S.K.; Giannella, R.A.
J. Biol. Chem. 256, 7744-7746, 1981
A:Title: Amino acid sequence of heat-stable enterotoxin produced by *Escherichia coli* pat
A:Reference number: A01823; MUID:81264141; PMID:7021541
A:Accession: A01823
A:Molecule type: protein
A:Residues: 1-18 <CHA>
A:Cross-references: UNIPROT:P01560
A:Experimental source: strain 18D, serotype 0.42:k86:H37
C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced by
C:Superfamily: heat-stable enterotoxin ST-1.
C:Keywords: enterotoxin; heat-stable protein
F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
F:5-10,6-14,9-17/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 0.00137 Length: 18
Score: 83.00 Matches: 12
Percent Similarity: 85.71% Conservative: 0
Best Local Similarity: 85.71% Mismatches: 2
Query Match: 65.87% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x QHEC2 (1-18)

Qy 13 TACTGCTGTGAATGTGTGTAATCTCTGTGTAACGGGTGC 54
|||||
Db 4 TyrCysCysGluLeuCysCysTyrProAlaCysAlaGlyCys 17
|||||

RESULT 8
A54534
heat-stable enterotoxin - Vibrio mimicus (fragment)
C:Species: Vibrio mimicus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996
C:Accession: A54534
R:Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.
FEMS Microbiol. Lett. 79, 105-110, 1991
A:Title: Purification and characterization of a heat-stable enterotoxin of *Vibrio mimicus*
A:Reference number: A54534
A:Accession: A54534
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <ARI>
C:Superfamily: heat-stable enterotoxin ST

Alignment Scores:
Pred. No.: 0.00269 Length: 17
Score: 81.00 Matches: 11
Percent Similarity: 92.31% Conservative: 1
Best Local Similarity: 84.62% Mismatches: 1
Query Match: 64.29% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x A54534 (1-17)

QY 16 TCCTGTGAATGTTGTAATCCTGCTTAAACGGGTGC 54
 |||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 3 CysCysGluileCysCysAsnProAlaCysPheGlyCys 15

RESULT 9

QHVCI

heat-stable enterotoxin ST precursor - Vibrio cholerae
 C:Species: Vibrio cholerae
 C:Date: 17-Mar-1987 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004
 A:Accession: A41469; A01824; S34466; S34465; S34463
 R:Ogawa, A.; Kato, J.; Watanabe, H.; Nair, B.G.; Takeda, T.
 Infect. Immun. 58, 3325-3329, 1990
 A:Title: Cloning and nucleotide sequence of a heat-stable enterotoxin gene from Vibrio
 A:Reference number: A41469; MUID:90382953; PMID:2205577
 A:Accession: A41469
 A:Molecule type: DNA
 A:Residues: 1-78 <OGA>
 A:CROSS-references: UNIPROT:P04429; GB:M85198; PIDN:AAA64889.1;
 R:Takao, T.; Shimonishi, Y.; Kobayashi, M.; Nishimura, O.; Arita, M.; Takeda, T.; Honda,
 FEBS Lett. 193, 250-254, 1985
 A:Title: Amino acid sequence of heat-stable enterotoxin produced by Vibrio cholerae non-
 A:Reference number: A01824; MUID:86056320; PMID:4065341
 A:Accession: A01824
 A:Molecule type: protein
 A:Residues: 62-78 <TAK>
 A:Experimental source: non-O:1 serovar
 R:Yoshino, K.; Miyachi, M.; Takao, T.; Bag, P.K.; Xiaozhe, H.; Nair, G.B.; Takeda, T.; S
 FEBS Lett. 326, 83-86, 1993
 A:Title: Purification and sequence determination of heat-stable enterotoxin elaborated b
 A:Reference number: S34463; MUID:93314823; PMID:8325391
 A:Accession: S34464
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 61-78 <Y03>
 A:Accession: S34466
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 51-78 <Y0S>
 A:Accession: S34465
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 60-78 <Y02>
 A:Accession: S34463
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 62-78 <Y04>
 C:Superfamily: heat-stable enterotoxin ST
 C:Keywords: enterotoxin; heat-stable protein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-61/Domain: signal sequence #status predicted <PRO>
 F:62-78/Product: heat-stable enterotoxin ST #status experimental <MAT>
 F:64-69,65-73,68-76/Disulfide bonds: #status predicted

Alignment Scores:
 Pred. No.: 0.00178 Length: 78
 Score: 81.00 Matches: 11
 Percent Similarity: 92.31% Conservative: 1
 Best Local Similarity: 84.62% Mismatches: 1
 Query Match: 64.29% Indels: 0
 DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x QHVCI (1-78)

QY 16 TCCTGTGAATGTTGTAATCCTGCTTAAACGGGTGC 54
 |||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 64 CysCysGluileCysCysAsnProAlaCysPheGlyCys 76

RESULT 10

S25659

heat-stable enterotoxin yst precursor - Yersinia enterocolitica
 C:Species: Yersinia enterocolitica
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C:Accession: S25659; A41474; A23114; S65849
 R:Ibrahim, A.; Liesack, W.; Pike, S.; Stackebrandt, E.
 FEMS Microbiol. Lett. 97, 63-66, 1992
 A:Title: The polymerase chain reaction: an epidemiological tool to differentiate between
 A:Reference number: S25659
 A:Accession: S25659
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-71 <IBR>
 A:CROSS-references: UNIPROT:P07593; EMBL:X65999; NID:948611; PIDN:CAA46801.1; PID:948612
 R:Delor, I.; Kaackenbeeck, A.; Wauters, G.; Cornelis, G.R.
 Infect. Immun. 58, 2983-2988, 1990
 A:Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-st
 A:Reference number: A41474; MUID:90354067; PMID:2201642
 A:Accession: A41474
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-47, 'S', '49-71
 A:CROSS-references: GB:U09235; NID:9487394; PIDN:AAA18472.1; PID:9487395
 R:Takao, T.; Tominega, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A
 Eur. J. Biochem. 152, 199-206, 1985
 A:Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced k
 A:Reference number: A23114; MUID:86004705; PMID:4043080
 A:Accession: A23114
 A:Molecule type: protein
 A:Residues: 54-71 <TAK>
 R:Mikulskis, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.
 Mol. Microbiol. 14, 905-915, 1994
 A:Title: Regulation of the Yersinia enterocolitica enterotoxin Yst gene. Influence of gro
 A:Reference number: S65849; MUID:95231297; PMID:7715452
 A:Accession: S65849
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-43 <MIK>
 A:CROSS-references: EMBL:U09235
 C:Genetics:
 A:Gene: yst
 C:Superfamily: heat-stable enterotoxin ST
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-41/Domain: propeptide #status predicted <PRO>
 F:42-71/Product: heat-stable enterotoxin yst #status predicted <MAT>
 Alignment Scores:
 Pred. No.: 0.00414 Length: 71
 Score: 78.50 Matches: 12
 Percent Similarity: 88.89% Conservative: 4
 Best Local Similarity: 66.67% Mismatches: 1
 Query Match: 62.30% Indels: 1
 DB: 2 Gaps: 1
 US-10-775-481A-4 (1-57) x S25659 (1-71)
 QY 4 AGTAGCAATTAAC---TCCTGTGAATGTTGTAATCCTGCTTAAACGGGTGC 54
 |||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 54 SerSerAspTrpAspCysCysAspValCysCysAsnProAlaCysAlaGlyCys 71
 RESULT 11
 S34671
 heat-stable enterotoxin - Vibrio cholerae (fragment)
 C:Species: Vibrio cholerae
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S34671
 R:Rossolini, G.M.; Lombardi, G.; Guglielmetti, P.
 submitted to the EMBL Data Library, July 1993
 A:Description: Detection of the Vibrio cholerae heat-stable enterotoxin gene by polymera
 A:Reference number: S34671
 A:Accession: S34671
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-65 <ROS>
 A:CROSS-references: UNIPROT:Q56643; EMBL:X74108
 C:Superfamily: heat-stable enterotoxin ST

Alignment Scores:

Pred. No.: 0.0959 Length: 65
 Score: 69.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 90.00% Mismatches: 0
 Query Match: 54.76% Indels: 0
 DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x S34671 (1-65)

Qy 16 TGCTGTGAATGTGTGTAATCCTCTGTGT 45

Db 55 CysCysGluIleCysCysAsnProAlaCys 64

RESULT 12

A45910
 ultra-high-sulfur keratin - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
 C:Accession: A45910
 R:McNab, A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.
 J. Invest. Dermatol. 92, 263-266, 1989
 A:Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.
 A:Reference number: A45910; MUID:89140394; PMID:2465353
 A:Accession: A45910
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-186 <MCN>
 A:Cross-references: UNIPROT:Q64526; GB:M27685; NID:g341749; PIDN:AAA81560.1; PID:g106681
 C:Superfamily: ultra-high-sulfur keratin

Alignment Scores:

Pred. No.: 0.608 Length: 186
 Score: 62.50 Matches: 10
 Percent Similarity: 54.55% Conservative: 2
 Best Local Similarity: 45.45% Mismatches: 3
 Query Match: 49.60% Indels: 7
 DB: 2 Gaps: 1

US-10-775-481A-4 (1-57) x A45910 (1-186)

Qy 13 TACTGCTGAATGTGTGTAATCCTCTGTGTACGGG-----51

Db 140 PheCysLeuAsnLeuCysCysGlnProAlaCysSerGlyProValThrCysThrArgThr 159

Qy 52 TGCTAT 57

Db 160 CysTyr 161

RESULT 13

JC4651
 uroguanylin precursor - human
 A:Alternate names: guanylyl cyclase activating peptide II
 C:Species: Homo sapiens (man)
 C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C:Accession: JC4651; S63702; S68052
 R:Miyaoto, M.; Nakazato, M.; Yamaguchi, H.; Date, Y.; Kojima, M.; Kangawa, K.; Matsuo, Biochem. Biophys. Res. Commun. 219, 644-648, 1996
 A:Title: Cloning and characterization of a cDNA encoding a precursor for human uroguanylin
 A:Reference number: JC4651; MUID:96193705; PMID:8605041
 A:Accession: JC4651
 A:Molecule type: mRNA
 A:Residues: 1-112 <MIY>
 A:Cross-references: UNIPROT:Q16661; GB:U34279; NID:g1236798; PIDN:AA50416.1; PID:g12367
 R:Hill, O.; Cetin, Y.; Cieslak, A.; Maegert, H.J.; Forssmann, W.G.
 Biochim. Biophys. Acta 1253, 146-149, 1995
 A:Title: A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): precursor
 A:Reference number: S63702; MUID:96106424; PMID:8519795
 A:Accession: S63702
 A:Molecule type: mRNA
 A:Residues: 1-112 <HLI>
 A:Cross-references: EMBL:Z50753; NID:g974823; PIDN:CAA90629.1; PID:g974824
 A:Experimental source: tissue colon

R:Hess, R.; Kuhn, M.; Schulz-Knappe, P.; Raida, M.; Fuchs, M.; Klodt, J.; Adermann, K.; FEBS Lett. 374, 34-38, 1995
 A:Title: GCAP-II: isolation and characterization of the circulating form of human uroguanylin
 A:Reference number: S68052; MUID:96049550; PMID:7589507
 A:Accession: S68052

A:Molecule type: protein
 A:Residues: 89-99,'X',101-102,'X',104-107,'X',109-110,'X',112 <HES>
 C:Comment: This protein, a member of the guanylin peptide family, is an endogenous activator of the guanylyl cyclase.

C:Superfamily: guanylin

C:Keywords: intestines

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-112/Product: uroguanylin #status predicted <MAT>

Alignment Scores:

Pred. No.: 2.2 Length: 112
 Score: 59.00 Matches: 10
 Percent Similarity: 68.75% Conservative: 1
 Best Local Similarity: 62.50% Mismatches: 5
 Query Match: 46.83% Indels: 0
 DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x JC4651 (1-112)

Qy 7 AGCAATTACTCTGTGAATGTGTGTAATCCTCTGTGTAAACGGGTGC 54

Db 96 AlaAsnAspAspCysGluLeuCysValAsnValAlaCysThrGlyCys 111

RESULT 14

JC7620
 guanylin precursor, long form - European eel
 C:Species: Anguilla anguilla (European eel)
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C:Accession: JC7620
 R:Comrie, W.M.; Cutler, C.P.; Cramb, G.
 Biochem. Biophys. Res. Commun. 281, 1078-1085, 2001
 A:Title: Cloning and expression of guanylin from the European eel (*Anguilla anguilla*).
 A:Reference number: JC7620; MUID:21139737; PMID:11243845
 A:Accession: JC7620
 A:Molecule type: mRNA
 A:Residues: 1-116 <COM>
 A:Cross-references: GB:AJ301673
 C:Comment: This protein, a member of a family of heat-stable peptides, is a potent extra-cellular osmoregulatory factor. It plays a role in osmoregulation in euryhaline teleosts.
 C:Superfamily: guanylin
 C:Keywords: heat-stable protein; osmoregulation
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-116/Product: guanylin precursor, long form #status predicted <MAT>
 F:33-39/Region: homologous #status predicted
 F:69-114/Region: highly conserved #status predicted

Alignment Scores:

Pred. No.: 3.03 Length: 116
 Score: 58.00 Matches: 8
 Percent Similarity: 75.00% Conservative: 1
 Best Local Similarity: 66.67% Mismatches: 3
 Query Match: 46.03% Indels: 0
 DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x JC7620 (1-116)

Qy 19 TGTGAATTGTGTGTAATCCTCTGTGTAAACGGGTGC 54

Db 104 CysGluIleCysAlaAsnAlaAlaCysThrGlyCys 115

RESULT 15

JC6548
 high sulfur protein B2F - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C:Accession: JC6548
 R:Mitsui, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Teuboi, R.; Ogawa, H.
 Gene 208, 123-129, 1998

A;Title: Structure and hair follicle-specific expression of genes encoding the rat high
 A;Reference number: JC6547; MUID:98201605; PMID:9524245
 A;Accession: JC6548
 A;Molecule type: DNA
 A;Residues: 1-122 <MIT>
 A;Cross-references: UNIPROT:070149; DBJ:AB003753; NID:G3046870; PIDN:BA25574.1; PID:G3
 C;Comment: This protein is a cysteine-rich, keratin associated protein.
 C;Genetics:
 A;Gene: b2F
 C;Superfamily: keratin high-sulfur matrix protein IIIA

Alignment Scores:
 Pred. No.: 9.42 Length: 122
 Score: 54.50 Matches: 9
 Percent Similarity: 68.75% Conservative: 2
 Best Local Similarity: 56.25% Mismatches: 4
 Query Match: 43.25% Indels: 1
 DB: 2 Gaps: 1

US-10-775-481A-4 (1-57) x JC6548 (1-122)

Qy 10 AATTACTGCTGTGAATTGTGTGTAATCCTCTGTGAACGGGTCTAT 57
 Db 106 SerTyrCysGlyGlnSerCysCysArgProAlaCys---CysCysTyr 120

Search completed: March 26, 2005, 17:51:44
 Job time : 26 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 26, 2005, 17:27:32 ; Search time 84 Seconds
(without alignments)

694.965 Million cell updates/sec

Title: US-10-775-481A-4

Perfect score: 126

Sequence: 1 aatagtagcaattactgtg.....ctgtttgaacgggtgtat 57

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_P/US1075481/runat_25032005_151018_7789/app_query.fasta_1.199
-DB=UniProt_03 -QMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=spect -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US1075481 @CGN 1 1 152 @runat_25032005_151018_7789 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	120	95.2	61 2 QVEG8	Qveg8 escherichia
2	120	95.2	72 1 HST2_ECOLI	Q47185 escherichia
3	120	95.2	72 1 HST3_ECOLI	P07965 escherichia
4	116	92.1	61 2 QSVG7	Q6veg7 escherichia
5	103	81.7	72 1 HST1_ECOLI	P01569 escherichia
6	98	77.8	18 2 Q7M0U3	Q7m0u3 citrobacter
7	95	75.4	61 2 QSVG9	Q6veg9 escherichia
8	89	70.6	72 1 HSTC_YEREN	OS0319 yersinia en
9	88	69.8	66 1 HST_YERKR	P31518 yersinia kr
10	85	67.5	71 1 HSTB_YEREN	P74977 yersinia en
11	83	65.9	18 1 HSTB_ECOLI	P01560 escherichia
12	81	64.3	17 2 Q9S581	Q9s581 vibrio chol
13	81	64.3	18 2 Q9S580	Q9s580 vibrio chol
14	81	64.3	19 2 Q9S579	Q9s579 vibrio chol
15	81	64.3	28 2 Q9S578	Q9s578 vibrio chol
16	81	64.3	78 1 HSTN_VIBCH	P04429 vibrio chol

17	81	64.3	78 1	HSTO_VIBCH	Q07425 vibrio chol
18	78.5	62.3	71 1	HSTA_YEREN	P07593 yersinia en
19	72	57.1	66 2	Q56643	Q56643 vibrio chol
20	72	57.1	78 2	Q93G01	Q93g01 vibrio mini
21	62.5	49.6	186 2	Q64526	Q64526 mus musculus
22	62.5	49.6	191 2	Q9D3H7	Q9d3h7 mus musculus
23	62.5	49.6	195 2	Q9D141	Q9d141 mus musculus
24	61	48.4	118 2	Q8WT16	Q8wt16 drosophila
25	61	48.4	197 2	Q86144	Q86144 dictyosteli
26	59	46.8	105 2	Q9BYP8	Q9byp8 homo sapien
27	59	46.8	112 1	GUAU_HUMAN	Q15661 homo sapien
28	58	46.0	106 1	GUAU_MOUSE	Q09051 mus musculus
29	58	46.0	106 1	GUAU_RAT	P07668 rattus norv
30	58	46.0	106 2	Q9QUQ3	Q9quq3 mus musculus
31	58	46.0	107 2	Q8R5G8	Q8r5g8 notomys ale
32	58	46.0	108 2	Q98T10	Q98t10 anguilla an
33	58	46.0	108 2	Q7ZZS0	Q7zzs0 anguilla ja
34	58	46.0	109 1	GUAU_DIDMA	Q28358 didelphis m
35	58	46.0	113 1	GUAU_PIG	O13009 sus scrofa
36	58	46.0	116 2	Q98TH9	Q98th9 anguilla an
37	58	46.0	167 2	Q9D122	Q9d122 mus musculus
38	57	45.2	111 1	GUAU_CAVPO	P70107 cavia porce
39	57	45.2	154 1	KR99_HUMAN	Q9byp9 homo sapien
40	56	44.4	168 2	Q9D732	Q9d732 mus musculus
41	56	44.4	426 2	Q67UU9	Q67uu9 oryza sativ
42	55.5	44.0	106 2	Q9QYU5	Q9qyu5 rattus norv
43	55	43.7	111 1	KR95_HUMAN	Q9byq1 homo sapien
44	55	43.7	154 1	KR94_HUMAN	Q9byq2 homo sapien
45	55	43.7	159 1	KR93_HUMAN	Q9byq3 homo sapien

ALIGNMENTS

RESULT 1

Q6VEG8 PRELIMINARY; PRT; 61 AA.
ID Q6VEG8
AC Q6VEG8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat-stable enterotoxin ST Ib (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C4046;
RX PubMed=15364995;
RA Reischl U., Yousef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
of heat-labile I and heat-stable I enterotoxin genes from
enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL; AY342058; AAQ92975.1;
DR GO; GO:0005976; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
FT NON TER 1
SQ SEQUENCE 61 AA; 6658 MW; 1D75955D7AF0DED2 CRC64;

Alignment Scores:
Pred. No.: 1.61e-09 Length: 61
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x Q6VEG8 (1-61)

OY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTGTGAACGGTGCTAT 57
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 43 AnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 61

RESULT 2

HST2_ECOLI ID HST2_ECOLI STANDARD; PRT; 72 AA.
 AC Q47185;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin A2 precursor (STA2).
 GN Name=sta2;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89108616; PubMed=2643580;
 RX Guzman-Verduzco L.M., Kupersztach Y.M.;
 RA "Rectification of two Escherichia coli heat-stable enterotoxin allele
 RT sequences and lack of biological effect of changing the carboxy-
 RL terminal tyrosine to histidine.";
 RL Infect. Immun. 57:645-648(1989).
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M18345; AAA23729.1; --
 DR PIR; JS0292; QHECIB.
 DR HSP; P01559; IETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Enterotoxin; Signal; Toxin.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 53 By similarity.
 FT PEPTIDE 54 72 Heat-stable enterotoxin A2.
 FT DISULFID 59 64 By similarity.
 FT DISULFID 60 68 By similarity.
 FT DISULFID 63 71 By similarity.
 SQ SEQUENCE 72 AA; 7895 MW; D87850306E05E260 CRC64;

Alignment Scores:
 Pred. No.: 1.6e-09 Length: 72
 Score: 120.00 Matches: 18
 Percent Similarity: 94.74% Conservative: 0
 Best Local Similarity: 94.74% Mismatches: 1
 Query Match: 95.24% Indels: 0
 DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x HST2_ECOLI (1-72)

OY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTGTGAACGGTGCTAT 57

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

54 AnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

RESULT 3

HST3_ECOLI ID HST3_ECOLI STANDARD; PRT; 72 AA.
 AC P07965; P26588;
 DT 01-AUG-1988 (Rel. 08, Created)

OY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTGTGAACGGTGCTAT 57

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

54 AnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

US-10-775-481A-4 (1-57) x HST2_ECOLI (1-72)

OY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTGTGAACGGTGCTAT 57

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

54 AnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

US-10-775-481A-4 (1-57) x HST2_ECOLI (1-72)

OY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTGTGAACGGTGCTAT 57

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

54 AnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

US-10-775-481A-4 (1-57) x HST2_ECOLI (1-72)

OY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTGTGAACGGTGCTAT 57

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

54 AnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

US-10-775-481A-4 (1-57) x HST2_ECOLI (1-72)

OY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTGTGAACGGTGCTAT 57

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

54 AnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin A3/A4 precursor (STA3/STA4) (ST-IB) (ST-H).
 GN Name=sta3; Synonyms=sta4;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89202548; PubMed=3071819;
 RX Sleglitz H., Cervantes L., Robledo R., Fonseca R., Covarrubias L.,
 RA Bolivar F., Kupersztach Y.M.;
 RA "Cloning, sequencing, and expression in Ficol-generated minicells of
 RT an Escherichia coli heat-stable enterotoxin gene.";
 RL Plasmid 20:42-53(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=153837-2;
 RX MEDLINE=83184648; PubMed=6341230;
 RA Moseley S.L., Hardy J.W., Huq M.I., Echeverria P., Falkow S.;
 RA "Isolation and nucleotide sequence determination of a gene encoding a
 RT heat-stable enterotoxin of Escherichia coli.";
 RL Infect. Immun. 39:1167-1174(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90273381; PubMed=2190361; DOI=10.1016/0041-0101(90)90085-L;
 RX Zhou X., Shen L.P., Chi C.W.;
 RA "Isolation and nucleotide sequence determination of a gene encoding a
 RT heat-stable enterotoxin of Escherichia coli.";
 RL Toxicon 28:453-456(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89108616; PubMed=2643580;
 RX Guzman-Verduzco L.M., Kupersztach Y.M.;
 RA "Rectification of two Escherichia coli heat-stable enterotoxin allele
 RT sequences and lack of biological effect of changing the carboxy-
 RL terminal tyrosine to histidine.";
 RL Infect. Immun. 57:645-648(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90034194; PubMed=2680769; DOI=10.1016/0378-1119(89)90182-0;
 RX Dwatakanath P., Visweswariah S.S., Subrahmanyam Y.V.B.K., Shanthi G.,
 RA Jagannatha H.M., Balganesht T.S.;
 RA "Cloning and hyperexpression of a gene encoding the heat-stable toxin
 RT of Escherichia coli.";
 RL Gene 81:219-226(1989).
 RN [6]
 RP SEQUENCE OF 54-72.
 RX MEDLINE=83105138; PubMed=6759126;
 RA Aimoto S., Takao T., Shimonishi Y., Hara S., Takeda T., Takeda Y.,
 RA Miwatani T.;
 RA "Amino-acid sequence of a heat-stable enterotoxin produced by human
 RT enterotoxigenic Escherichia coli.";
 RL Eur. J. Biochem. 129:257-263(1982).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
 RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
 RA Miwatani T., Takeda Y.;
 RA "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)
 RT produced by a human strain of enterotoxigenic Escherichia coli.";
 RL FEBS Lett. 215:165-170(1987).
 RN [8]
 RP PROCESSING.
 RX MEDLINE=90251166; PubMed=2187146;
 RA Rasheed J.K., Guzman-Verduzco L.M., Kupersztach Y.M.;
 RA "Two precursors of the heat-stable enterotoxin of Escherichia coli:
 RT evidence of extracellular processing.";
 RL Mol. Microbiol. 4:265-273(1990).
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC -----
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 CC -----

DR EMBL: J03311; AAA24652.1; -
 DR EMBL: M34916; AAA23990.1; -
 DR EMBL: M18346; AAA23730.1; -
 DR EMBL: M29255; AAA24686.1; -
 DR PIR: JS0292; QHECIB.
 DR PIR: JT0373; QHEC4.
 DR HSSP: P01559; 1ETN.
 DR InterPro: IPR001489; Enterotoxin_HS.
 DR Pfam: PF02048; Enterotoxin_HS; 1.
 DR PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
 KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
 FT SIGNAL 1 19
 FT PROPEP 20 53
 FT PEPTIDE 54 72 Heat-stable enterotoxin A3/A4.
 FT DISULFID 59 64
 FT DISULFID 60 68
 FT DISULFID 63 71
 FT CONFLICT 19 19 A -> P (in Ref. 2).
 SQ SEQUENCE 72 AA; 7909 MW; 1C5C9292BFCBA6BA CRC64;

Alignment Scores:

Pred. No.: 1.6e-09 Length: 72
 Score: 120.00 Matches: 18
 Percent Similarity: 94.74% Conservative: 0
 Best Local Similarity: 94.74% Mismatches: 1
 Query Match: 95.24% Indels: 0
 DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x HST1_ECOLI (1-72)

Qy 1 AATAGTACCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTTGTAAACGGGTGCTAT 57
 Db 54 AsnSerSerAsnTyCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 72

RESULT 4

Q6VEG7
 ID Q6VEG7 PRELIMINARY; PRT; 61 AA.
 AC Q6VEG7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heat-stable enterotoxin ST 1b (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R544;
 RX PubMed=15364995;
 RA Reischl U., Yousef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
 RA "Real-time fluorescence PCR assays for detection and characterization
 RA of heat-labile I and heat-stable I enterotoxin genes from
 RA enterotoxigenic Escherichia coli";
 RL J. Clin. Microbiol. 42:4092-4100(2004).
 DR EMBL: AY342059; AAQ92976.1; -
 DR GO: GO:0005776; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001489; Enterotoxin_HS.
 DR Pfam: PF02048; Enterotoxin_HS; 1.
 DR PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
 FT NON_TER 1 1

SQ SEQUENCE 61 AA; 6556 MW; 89788D3FAB3DCA0A CRC64;

Alignment Scores:

Pred. No.: 6.59e-09 Length: 61
 Score: 116.00 Matches: 17
 Percent Similarity: 89.47% Conservative: 0
 Best Local Similarity: 89.47% Mismatches: 2
 Query Match: 92.06% Indels: 0
 DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x Q6VEG7 (1-61)

Qy 1 AATAGTACCAATTACTGCTGTGAATTGTTGTTGTAATCTGCTTGTAAACGGGTGCTAT 57
 Db 43 AsnGlySerAsnTyCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 61

RESULT 5

HST1_ECOLI
 ID HST1_ECOLI STANDARD; PRT; 72 AA.
 AC P01559; Q47653;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Heat-stable enterotoxin ST-1A/ST-P precursor.
 GN Name=stai;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn1681;
 RA So M., McCarthy B.J.;
 RA "Nucleotide sequence of the bacterial transposon Tn1681 encoding a
 RA heat-stable (ST) toxin and its identification in enterotoxigenic
 RA Escherichia coli strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:4011-4015(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O42:K86:H37 / 18D / ETEC;
 RX MEDLINE=90368614; PubMed=2203756;
 RA Dallas W.S.;
 RA "The heat-stable toxin I gene from Escherichia coli 18D";
 RN J. Bacteriol. 172:5490-5493(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85249571; PubMed=2990268;
 RA Sekizaki T., Akashi H., Terakado N.;
 RA "Nucleotide sequences of the genes for Escherichia coli heat-stable
 RA enterotoxin I of bovine, avian, and porcine origins";
 RL Am. J. Vet. Res. 46:909-912(1985).
 RN [4]
 RP DISULFIDE BONDS.
 RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
 RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
 RA Miwatani T., Takeda Y.;
 RA "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)
 RA produced by a human strain of enterotoxigenic Escherichia coli";
 RL FEBS Lett. 215:165-170(1987).
 RN [5]
 RP PROCESSING.
 RX MEDLINE=90368584; PubMed=2203746;
 RA Okamoto K., Takahara M.;
 RA "Synthesis of Escherichia coli heat-stable enterotoxin Stp as a pre-
 RA pro form and role of the pro sequence in secretion";
 RL J. Bacteriol. 172:5260-5265(1990).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (0.89 ANGSTROMS) OF 59-71.
 RX MEDLINE=94312375; PubMed=8038153;
 RA Sato T., Ozaki H., Hata Y., Kitagawa Y., Katsube Y., Shimonishi Y.;
 RA "Structural characteristics for biological activity of heat-stable
 RA enterotoxin produced by enterotoxigenic Escherichia coli: X-ray

RT crystallography of weakly toxic and nontoxic analogs.";
 RL Biochemistry 33:8641-8650(1994).
 CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC -----
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EMBL; V00612; CAA23883.1; -;
 DR EMBL; M58746; AAA62776.1; -;
 DR EMBL; M25607; AAA24653.1; -;
 DR PIR; A01822; QHEC1.
 DR PDB; 1ETL; X-ray; @=59-71.
 DR PDB; 1ETM; X-ray; @=-;
 DR PDB; 1ETN; X-ray; @=-;
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 DR 3D-structure; Enterotoxin; Signal; Toxin; Transposable element.
 FT SIGNAL 1 19
 FT PROPEP 20 54
 FT PEPTIDE 55 72 Heat-stable enterotoxin ST-1A/ST-P.
 FT DISULFID 59 64
 FT DISULFID 60 68
 FT DISULFID 63 71
 FT CONFLICT 70 70 G -> P (in Ref. 3).
 FT TURN 61 62
 FT TURN 66 67
 FT TURN 69 70
 SQ SEQUENCE 72 AA; 8075 MW; 92E8B766B3988264 CRC64;

Alignment Scores:
 Pred. No.: 6.38e-07 Length: 72
 Score: 103.00 Matches: 15
 Percent Similarity: 89.47% Conservative: 2
 Best Local Similarity: 78.95% Mismatches: 2
 Query Match: 81.75% Indels: 0
 DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x HST1_ECOLI (1-72)

QY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTAATCTCTGTAAACGGGTGCTAT 57
 |||:::|
 Db 54 AsnAsnThrPheTyrCysGluLeuCysCysAsnProAlaCysAlaGlyCysTyr 72
 |||:::|

RESULT 6
 Q7M0U3 PRELIMINARY; PRT; 18 AA.
 ID Q7M0U3
 AC Q7M0U3
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Heat-stable enterotoxin ST-1a.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=89108617; PubMed=2912902;
 RA Guarino A., Giannella R., Thompson M.R.;
 RT "Citrobacter freundii produces an 18-amino-acid heat-stable
 RT enterotoxin identical to the 18-amino-acid Escherichia coli heat-
 RT stable enterotoxin (St 1a).";
 RL Infect. Immun. 57:649-652(1989).

DR PIR; A60103; A60103;
 DR HSPP; P01559; IETN.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 SQ SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;
 Alignment Scores:
 Pred. No.: 3.84e-06 Length: 18
 Score: 98.00 Matches: 14
 Percent Similarity: 93.33% Conservative: 0
 Best Local Similarity: 93.33% Mismatches: 1
 Query Match: 77.78% Indels: 0
 DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x Q7M0U3 (1-18)

QY 13 TACTGCTGTGAATTGTTGTAATCTCTGTAAACGGGTGCTAT 57
 |||:::|
 Db 4 TyrCysCysGluLeuCysCysAsnProAlaCysAlaGlyCysTyr 18
 |||:::|

RESULT 7
 Q6VEG9 PRELIMINARY; PRT; 61 AA.
 ID Q6VEG9
 AC Q6VEG9
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heat-stable enterotoxin ST-1a (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F7682;
 RX PubMed=15364995;
 RA Reischl U., Youseef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
 RT "Real-time fluorescence PCR assays for detection and characterization
 RT of heat-labile I and heat-stable I enterotoxin genes from
 RT enterotoxigenic Escherichia coli.";
 RL J. Clin. Microbiol. 42:4092-4100(2004).
 DR EMBL; AY342057; RAQ92974.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 FT NON_TER 1
 SQ SEQUENCE 61 AA; 6927 MW; 646D4AE2F899D957 CRC64;

Alignment Scores:
 Pred. No.: 1.07e-05 Length: 61
 Score: 95.00 Matches: 14
 Percent Similarity: 84.21% Conservative: 2
 Best Local Similarity: 73.68% Mismatches: 3
 Query Match: 75.40% Indels: 0
 DB: 2 Gaps: 0

US-10-775-481A-4 (1-57) x Q6VEG9 (1-61)

QY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTAATCTCTGTAAACGGGTGCTAT 57
 |||:::|
 Db 43 AsnAsnThrPheTyrCysGluLeuCysCysAsnProAlaCysAlaProCysTyr 61
 |||:::|

RESULT 8
 HSTC_YEREN
 ID HSTC_YEREN STANDARD; PRT; 72 AA.
 AC O50319;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

```

DE Heat-stable enterotoxin C precursor (Y-STC).
GN Name=YstC;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-11;
RX MEDLINE=97202479; PubMed=9049998; DOI=10.1006/mpat.1996.0094;
RA Huang X., Yoshino K., Nakao H., Takeda T.;
RT "Nucleotide sequence of a gene encoding the novel Yersinia
RT enterocolitica heat-stable enterotoxin that includes a pro-region-like
RT sequence in its mature toxin molecule.";
RL Microb. Pathog. 22:89-97(1997).
RN [2]
RP SEQUENCE OF 20-72.
RC STRAIN=Serotype O:3;
RX MEDLINE=95245844; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
RA Yoshino K., Takao T., Huang X., Murata H., Nakao H., Takeda T.,
RA Shimonishi Y.;
RT "Characterization of a highly toxic, large molecular size heat-stable
RT enterotoxin produced by a clinical isolate of Yersinia
RT enterocolitica.";
RL FEBS Lett. 362:319-322(1995).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells. Highly toxic.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC
CC EMBL; D63578; BAA23656.1; -.
DR HSP; P01559; 1ETN.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19
FT CHAIN 20 72 Heat-stable enterotoxin C.
FT DISULFID 60 65 By similarity.
FT DISULFID 61 69 By similarity.
FT DISULFID 64 72 By similarity.
SQ SEQUENCE 72 AA; 7639 MW; 7C0D83893C2F981D CRC64;

Alignment Scores:
Pred. No.: 8.83e-05 Length: 72
Score: 89.00 Matches: 13
Percent Similarity: 83.33% Conservative: 2
Best Local Similarity: 72.22% Mismatches: 3
Query Match: 70.63% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x HSTC_YEREN (1-72)

QY 1 AATAGTAGCAATTAAGTCTGTGAATGTTGTGAATCTGCTGTGAACGGGTGC 54
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
55 AsnAspTrpAspTrpCysCysGluLeuCysCysAsnProAlaCysPheGlyCys 72
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
HST_YERKR
ID _HST_YERKR STANDARD; PRT; 66 AA.
AC P31518;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Heat-stable enterotoxin precursor.
GN Name=Yst;
OS Yersinia kristensenii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=28152;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP490 / Serotype O:12,25;
RA Ibrahim A., Liesack W., Stackebrandt E.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC EMBL; X69218; CAA49152.1; -.
DR PIR; S31652; S31652.
DR HSP; P01559; 1ETN.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Enterotoxin; Signal.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 50
FT CHAIN 51 66 Heat-stable enterotoxin (By similarity).
FT DISULFID 54 59 By similarity.
FT DISULFID 55 63 By similarity.
FT DISULFID 58 66 By similarity.
SQ SEQUENCE 66 AA; 7068 MW; 27BE7006675CC075 CRC64;

Alignment Scores:
Pred. No.: 0.000126 Length: 66
Score: 88.00 Matches: 12
Percent Similarity: 93.75% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 69.84% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x HST_YERKR (1-66)

QY 7 AGCAATTACTGCTGTGAATGTTGTGAATCTGCTGTGAACGGGTGC 54
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
51 SerAspTrpCysCysGluValCysCysAsnProAlaCysAlaGlyCys 66
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
HST_YEREN
ID _HST_YEREN STANDARD; PRT; 71 AA.
AC P74977;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin B precursor (Y-STB).
GN Name=YstB;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=84-50 / Serotype O:5;
RX MEDLINE=98008784; PubMed=9344780; DOI=10.1006/mpat.1997.0146;
RA Ramamurthy T., Yoshino K., Huang X., Nair G.B., Carniel E.,
RA Maruyama T., Fukushima H., Takeda T.;

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RESULT 13
Q9R580 PRELIMINARY; PRT; 18 AA.
AC Q9R580;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE 01-ST-2, VC-H-ST=HEAT-stable enterotoxin.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE.
RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
RA Takeda T., Shimonishi Y.;
RT "Purification and sequence determination of heat-stable enterotoxin
RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
RT O1.";
RL FEBS Lett. 326:83-86(1993).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 18 AA; 1934 MW; 3080692D018D601C CRC64;

Alignment Scores:
Pred. No.: 0.00153 Length: 18
Score: 81.00 Matches: 11
Percent Similarity: 92.31% Conservative: 1
Best Local Similarity: 84.62% Mismatches: 1
Query Match: 64.29% Indels: 0
DB: 2 Gaps: 0

US-10-775-481a-4 (1-57) x Q9R580 (1-18)

Qy 16 TGCTGTGAATTGTTGTAATCCTGCTGTGTAACGGGTGC 54
|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 CysCysGlutlleCysCysAsnProAlaCysPheGlyCys 16

RESULT 14
Q9R579 PRELIMINARY; PRT; 19 AA.
AC Q9R579;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE 01-ST-3=HEAT-stable enterotoxin.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE.
RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
RA Takeda T., Shimonishi Y.;
RT "Purification and sequence determination of heat-stable enterotoxin
RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
RT O1.";
RL FEBS Lett. 326:83-86(1993).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 19 AA; 2048 MW; 308015F1A18D601C CRC64;

Alignment Scores:
Pred. No.: 0.00153 Length: 19
Score: 81.00 Matches: 11
Percent Similarity: 92.31% Conservative: 1
Best Local Similarity: 84.62% Mismatches: 1
Query Match: 64.29% Indels: 0
DB: 2 Gaps: 0

```

```

Percent Similarity: 92.31% Conservative: 1
Best Local Similarity: 84.62% Mismatches: 1
Query Match: 64.29% Indels: 0
DB: 2 Gaps: 0

US-10-775-481a-4 (1-57) x Q9R579 (1-19)

Qy 16 TGCTGTGAATTGTTGTAATCCTGCTGTGTAACGGGTGC 54
|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 CysCysGlutlleCysCysAsnProAlaCysPheGlyCys 17

RESULT 15
Q9R578 PRELIMINARY; PRT; 28 AA.
AC Q9R578;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE 01-ST-4=HEAT-stable enterotoxin.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE.
RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
RA Takeda T., Shimonishi Y.;
RT "Purification and sequence determination of heat-stable enterotoxin
RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
RT O1.";
RL FEBS Lett. 326:83-86(1993).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 28 AA; 3080 MW; 25ECADAFBC57DB72 CRC64;

Alignment Scores:
Pred. No.: 0.00151 Length: 28
Score: 81.00 Matches: 11
Percent Similarity: 92.31% Conservative: 1
Best Local Similarity: 84.62% Mismatches: 1
Query Match: 64.29% Indels: 0
DB: 2 Gaps: 0

US-10-775-481a-4 (1-57) x Q9R578 (1-28)

Qy 16 TGCTGTGAATTGTTGTAATCCTGCTGTGTAACGGGTGC 54
|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 14 CysCysGlutlleCysCysAsnProAlaCysPheGlyCys 26

```

Search completed: March 26, 2005, 17:50:43
Job time : 84 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:35:58 ; Search time 20.8029 Seconds
(without alignments)
353.241 Million cell updates/sec

Title: US-10-775-481A-5

Perfect score: 126
Sequence: 1 NSSNYCCLCNACNGCY 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	19	2 AAR85948	Aar85948 ST Ib rec
2	126	100.0	19	2 RAY40510	Asy40510 ST recept
3	126	100.0	19	8 ADR45825	Adr45825 Amino aci
4	120	95.2	19	2 AAR95923	Aar95923 Enterotox
5	120	95.2	19	2 RAY02386	Asy02386 Heat stab
6	120	95.2	19	2 RAY23608	Aay23608 Escherich
7	120	95.2	19	2 RAY06972	Asy06972 E. coli h
8	120	95.2	19	2 RAY02398	Asy02398 Heat stab
9	120	95.2	19	4 AAM51879	Aam51879 Human the
10	120	95.2	19	6 AAO16204	Aao16204 E coli sm
11	120	95.2	19	6 ABG74825	Abg74825 E. coli h
12	120	95.2	19	7 ADC14120	Adc14120 Heat stab
13	120	95.2	19	8 ADR48340	Adr48340 Bacterial
14	120	95.2	19	8 ADR48359	Adr48359 Analgesic
15	120	95.2	19	8 ADR48398	Adr48398 Peptide u
16	120	95.2	19	8 ADR48329	Adr48329 E. coli S
17	120	95.2	21	8 ADR48372	Adr48372 Analgesic
18	120	95.2	21	8 ADR48413	Adr48413 GC-C acti
19	120	95.2	72	2 AAR20352	Aar20352 Sequence
20	120	95.2	72	2 AAR71975	Aar71975 E. coli s
21	120	95.2	72	8 ADR48356	Adr48356 Immature
22	118	93.7	19	8 ADR48451	Adr48451 GC-C acti
23	118	93.7	19	8 ADR48453	Adr48453 GC-C acti
24	118	93.7	19	8 ADR48302	Adr48302 GC-C acti
25	118	93.7	19	8 ADR48304	Adr48304 GC-C acti

26	117	92.9	19	8 ADR48310	Adr48310 GC-C acti
27	117	92.9	19	8 ADR48459	Adr48459 GC-C acti
28	116	92.1	19	7 ADC14123	Adc14123 Modified
29	116	92.1	19	7 ADC14121	Adc14121 Modified
30	116	92.1	19	8 ADR48360	Adr48360 Analgesic
31	116	92.1	19	8 ADR48305	Adr48305 GC-C acti
32	116	92.1	19	8 ADR48454	Adr48454 GC-C acti
33	116	92.1	19	8 ADR48404	Adr48404 GC-C acti
34	116	92.1	21	8 ADR48415	Adr48415 GC-C acti
35	116	92.1	21	8 ADR48373	Adr48373 Analgesic
36	116	92.1	21	8 ADR48374	Adr48374 Analgesic
37	116	92.1	21	8 ADR48414	Adr48414 GC-C acti
38	115	91.3	19	4 AAB83216	Aab83216 Escherich
39	115	91.3	19	8 ADR48446	Adr48446 GC-C acti
40	115	91.3	19	8 ADR48361	Adr48361 Analgesic
41	115	91.3	19	8 ADR48442	Adr48442 GC-C acti
42	115	91.3	19	8 ADR48293	Adr48293 GC-C acti
43	115	91.3	19	8 ADR48401	Adr48401 Peptide u
44	115	91.3	19	8 ADR48297	Adr48297 GC-C acti
45	115	91.3	19	8 ADR48308	Adr48308 GC-C acti

ALIGNMENTS

RESULT 1

AAR85948
ID AAR85948 standard; peptide; 19 AA.
XX
AC AAR85948;
XX
DT 19-JAN-1996 (first entry)
XX
DE ST Ib receptor ligand portion.
XX
KW ST; receptor; ligand; heat-stable toxin; conjugate; imaging; cancer;
KW colorectal; metastasis.
XX
OS Escherichia coli.
XX
PN W09511694-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012232.
XX
PR 26-OCT-1993; 93US-00141892.
PR 13-SEP-1994; 94US-00305056.
XX
(UYJE-) UNIV JEFFERSON THOMAS.
Waldman SA;
XX
WPI; 1995-178646/23.
Conjugated cpds. which specifically bind to colorectal cancer cells -
comprise heat-stable toxin receptor binding moiety and active moiety
which may be a therapeutic agent or a radioactive agent.
Claim 3; Page 116; 133pp; English.

New conjugated compounds are provided which consist of (1) an ST receptor binding moiety and (2) an active moiety which is a radio- stable agent. 'ST' refers to a heat stable toxin produced by E.coli and other organisms. Especially the radiostable agent is a therapeutic agent (e.g. methotrexate, doxorubicin, mitomycin), imaging agent (e.g. radioactive isotope) or nucleic acid; and the compound is used for the detection, imaging or treatment of colorectal tumours, particularly metastasised tumours. The present sequence is a specific example of an ST receptor binding peptide which can be used in the conjugate

Sequence 19 AA;

Query Match 100.0%; Score 126; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
 DB 1 NSSNYCCCLCCNPACNGCY 19

RESULT 2
 AAY40510
 ID AAY40510 standard; peptide; 19 AA.
 XX
 AC AAY40510;
 XX
 DT 03-DEC-1999 (first entry)
 XX
 DE ST receptor peptide ST 1b.
 XX
 KW Conjugated compound; ST receptor; heat-stable; toxin; colorectal cancer.
 XX
 OS Escherichia coli.
 XX
 PN US5962220-A.
 XX
 PD 05-OCT-1999.
 XX
 PF 06-JUN-1995; 95US-00467920.
 XX
 PR 26-OCT-1993; 93US-00141892.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Waldman SA;
 XX
 DR WPI; 1999-571264/48.
 XX
 DR N-PSDB; AAZ07541.
 XX
 PT Conjugated compound comprising a receptor moiety and active moiety,
 XX useful for the treatment/prevention of colorectal cancer.
 XX
 PS Claim 1; Col 21-22; 23pp; English.
 XX

The invention relates to a conjugated compound that comprises a ST (heat-stable toxin) receptor moiety selected from one of the sequences shown in CC
 CC AAY40508-Y40559 and an active moiety (antisense molecule). The compound CC
 CC is useful for the treatment of colorectal cancer. The use of the CC
 CC conjugated compound is advantageous compared to antibodies since it binds CC
 CC specifically to colorectal cells and has no toxic effect on normal cells. CC
 CC The present sequence represents the amino acid sequence of a ST receptor CC
 CC peptide ST 1b
 XX
 XX Sequence 19 AA;

Query Match 100.0%; Score 126; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
 DB 1 NSSNYCCCLCCNPACNGCY 19

RESULT 3
 ADR45825
 ID ADR45825 standard; peptide; 19 AA.
 XX
 AC ADR45825;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Amino acid sequence of heat stable toxin ST 1b.
 XX
 XX

KW heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
 KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
 KW ST 1b.
 XX
 OS Unidentified.
 XX
 PN WO2004071436-A2.
 XX
 PD 26-AUG-2004.
 XX
 PF 10-FEB-2004; 2004WO-US003765.
 XX
 PR 10-FEB-2003; 2003US-0446730P.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;
 XX
 DR WPI; 2004-615913/59.
 XX
 DR N-PSDB; ADR45824.
 XX

Increasing ST receptor molecules on the surface of a colorectal, gastric or esophageal cancer cell to treat these cancers comprises administering ST receptor ligand molecules that bind to ST receptors on the surface of the cancer cell.

Claim 6; SEQ ID NO 5; 97pp; English.

The specification describes a method for increasing the number of heat stable toxin (ST) receptor molecules on the surface of a metastasised colorectal cancer cell. The method comprises administering, by continuous infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight per hour for at least 6 hours, where ST receptor ligand molecules bind to ST receptors on the surface of the cancer cell in the individual and the number of ST receptor molecules on the surface of the cancer cell is increased. Therapeutic compositions comprising components which target ST receptors can then be used to inhibit proliferation of the colorectal, gastric and oesophageal cells. This method may be used for treating individuals that have diseases that affect colorectal, gastric and oesophageal cells, including colorectal, gastric or oesophageal cancers. The present sequence represents a ST, designated ST 1b, which is used as the ST receptor ligand in the method of the invention.

Query Match 100.0%; Score 126; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
 DB 1 NSSNYCCCLCCNPACNGCY 19

RESULT 4
 AAR95923
 ID AAR95923 standard; peptide; 19 AA.
 XX
 AC AAR95923;
 XX
 DT 14-JAN-1997 (first entry)
 XX
 DE Enterotoxigenic E. coli STa protein antigen.
 XX
 KW Mucosal binding composition; mucosal binding polypeptide; antigen;
 KW non-viral pathogen; sexually transmitted disease; administration;
 KW vaginal; rectal; oral; immune response; secretory immunity; mucous;
 KW enterotoxigenic; STa protein.
 XX
 OS Escherichia coli.
 XX
 PN WO9616178-A1.
 XX

PD 30-MAY-1996.
 XX
 PF 17-NOV-1995; 95WO-GB002708.
 XX
 PR 17-NOV-1994; 94US-00342241.
 XX
 PA (LEBE/) LEBENS M R.
 PA (HOLM/) HOLMGREN J R.
 XX
 PI Lebens MR, Holmgren JR;
 XX
 DR WPI; 1996-268614/27.
 XX
 XX Mucosal binding compositions for generating mucosal immune response -
 PT comprises mucosal binding peptide, pref. derived from cholera toxin, and
 PT an antigen, e.g. derived from E. coli, HIV, etc.
 XX
 PS Claim 36; Page 44; 65pp; English.
 XX
 CC A novel mucosal binding compsn. (MBC) comprises a mucosal binding
 CC polypeptide linked to at least 1 antigen from a non-viral pathogen, which
 CC causes a sexually transmitted disease (STD), e.g. the present
 CC enterotoxigenic E. coli Sta protein antigen. The MBC, which is
 CC administered vaginally, rectally or orally, generates a mucosal immune
 CC response against the viral STD by allowing for the prodn. of high levels
 CC of secretory immunity, which forms the 1st line of defence against the
 CC majority of STD
 XX
 SQ Sequence 19 AA;

 Query Match 95.2%; Score 120; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 NSSNYCCELCCNPACNGCY 19
 |||||
 Db 1 NSSNYCCELCCNPACTGCT 19
 |||||

 RESULT 5
 AAY02386
 ID AAY02386 standard; peptide; 19 AA.
 XX
 AC AAY02386;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Heat stable ST enterotoxin Sth.
 XX
 KW Selection; candidate drug; cell receptor binding; affinity;
 KW biological receptor; rational drug design; combinatorial drug design;
 KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
 KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
 XX
 OS Escherichia coli.
 XX
 PN WO9909416-A2.
 XX
 PD 25-FEB-1999.
 XX
 PF 20-AUG-1998; 98WO-GB002504.
 XX
 PR 20-AUG-1997; 97GB-00017652.
 XX
 PA (NYCO-) NYCOMED IMAGING AS.
 PA (COCK/) COCKRAIN J.
 XX
 PI Wolfe HR;
 XX
 DR WPI; 1999-181156/15.
 XX
 XX Method of drug selection - and use of an acetamidomethyl-protected
 PT polymer as a substrate in the solid state synthesis of an oligopeptide.

XX Disclosure; Page 1-2; 38pp; English.
 XX
 CC The specification describes a method for selecting a candidate drug
 CC compound having affinity for biological receptors. The method uses a
 CC combination of rational and combinatorial drug design techniques. At
 CC least 1 residue in the original cell receptor binding peptide is modified
 CC to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
 CC mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method
 CC is used for identification of a candidate receptor antagonist or agonist.
 CC The present peptide is a cell receptor binding peptide, and can thus be
 CC used as a starting point for identification of candidate drug compounds,
 CC using the method of the invention
 XX
 SQ Sequence 19 AA;

 Query Match 95.2%; Score 120; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 NSSNYCCELCCNPACNGCY 19
 |||||
 Db 1 NSSNYCCELCCNPACTGCT 19
 |||||

 RESULT 6
 AAY29608
 ID AAY29608 standard; peptide; 19 AA.
 XX
 AC AAY29608;
 XX
 DT 15-OCT-1999 (first entry)
 XX
 DE Escherichia coli heat stable ST enterotoxin Sth.
 XX
 KW Heat stable ST enterotoxin; immunoreagent; radiological therapy;
 KW diagnosis; ST receptor binding moiety; macrocyclic complexing agent;
 KW tumour; infectious diarrhoeal disease; diarrhoea.
 XX
 OS Escherichia coli.
 XX
 PN WO9939748-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 08-FEB-1999; 99WO-GB000396.
 XX
 PR 06-FEB-1998; 98US-00020233.
 XX
 PA (NYCO-) NYCOMED IMAGING AS.
 PA (MATT/) MATTHEWS D P.
 XX
 PI Snow RA, Dalecki DJ, Shah C, Black C, Wolfe H;
 XX
 DR WPI; 1999-494219/41.
 XX
 XX Macrocyclic complexing agents containing linked 2,6-pyridinylene nuclei
 PT as components of targeting immunoreagents binding to ST receptor.
 XX
 PS Disclosure; Page 39; 79pp; English.
 XX
 CC The present invention describes targeting immunoreagents (TI's)
 CC comprising a metal ion and a residue of a macrocyclic complexing agent
 CC (MCA). TI's are of use in diagnostic imaging and therapy of specific
 CC disease sites in a patient, using either radioactive, magnetic resonance,
 CC or fluorescent means of detection or use of the metal ion; alternatively,
 CC a substituent of these types may be introduced, e.g. radioactive iodine,
 CC to perform the same function. Most notable is the imaging and
 CC radiological therapy of tumours. In addition, a variety of bacteria,
 CC including Escherichia coli, Vibrio cholerae, Citrobacter freundii, and
 CC Yersinia enterocolitica, bind to ST receptors and cause infectious
 CC diarrhoeal diseases, particularly in pediatrics and in developing
 CC countries. These types of diarrhoea can also be treated using TI's. TI's

CC may specifically used to treat cancers and also be used as an
 CC anti-diarrhoeal agent. TI's are free from the various disadvantages of
 CC prior art reagents, including rapid destruction and/or excretion,
 CC instability in storage, and protein degradation. There is no perturbation
 CC of protein reactive groups at the pyridyl chelating site. AAY29607 to
 CC AAY29612 represent examples of heat stable ST enterotoxins given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 AA;

Query Match 95.2%; Score 120; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACTGCGY 19
 DB 1 NSSNYCCCLCCNPACTGCGY 19

RESULT 7
 AAY06972
 ID AAY06972 standard; peptide; 19 AA.
 XX AAY06972;
 AC
 XX 02-JUL-1999 (first entry)
 DT
 XX E. coli heat stable ST enterotoxin peptide Sth.
 DE
 XX Targeting immunoreagent; metal ion; immunoreactive; terpyridine; tumour;
 KW complexing agent; diagnostic imaging; radiological treatment; yttrium;
 KW therapeutic; radiation toxicity; heat stable; ST enterotoxin.
 XX
 XX Escherichia coli.
 XX
 XX WO9921587-A1.
 XX
 XX 06-MAY-1999.
 XX
 XX 15-OCT-1998; 98WO-GB003102.
 XX
 XX 15-OCT-1997; 97US-00951144.
 XX
 XX (NYCO-) NYCOMED IMAGING AS.
 XX (MATT/) MATTHEWS D P.
 XX
 XX Wolfe H, Delecki DJ, Yu S;
 XX WPI; 1999-302905/25.
 DR
 XX Targeting immunoreagent for diagnostic imaging and therapeutic
 PT compositions.
 PT
 XX Claim 16; Page 50; 57pp; English.

PS The invention provides a targeting immunoreagent that comprises a metal
 CC ion and an immunoreactive group covalently bonded to a terpyridine
 CC complexing agent of a specified formula. The immunoreagent is useful in
 CC diagnostic imaging and therapeutic compositions. The immunoreagent is
 CC used for radiological treatment of tumours. When the immunoreagent
 CC contains yttrium, the radiation toxicity is lower compared with other
 CC yttrium chelators. The immunoreagent is not rapidly metabolized and does
 CC not disperse and efficiently forms covalent bonds with proteins and other
 CC biological molecules. The immunoreagent has good emission characteristics
 CC and are easily spectrophotometrically analysed. Protein conjugates can be
 CC stored for metal complexing without activation steps that degrade
 CC protein. The terpyridine complexing agent rapidly complex with metals and
 CC the obtained chelates have good stability. Sequences AAY06971-976
 CC represent examples of heat stable ST enterotoxin peptides that can be
 CC used as the immunoreactive group in the immunoreagent of the invention
 XX
 SQ Sequence 19 AA;

Query Match 95.2%; Score 120; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACTGCGY 19
 DB 1 NSSNYCCCLCCNPACTGCGY 19

RESULT 8
 AAY02398
 ID AAY02398 standard; peptide; 19 AA.
 XX AAY02398;
 AC
 XX 09-JUL-1999 (first entry)
 DT
 XX Heat stable ST enterotoxin Sth.
 DE
 XX
 XX Selection; candidate drug; cell receptor binding; affinity;
 KW biological receptor; rational drug design; combinatorial drug design;
 KW receptor antagonist; receptor agonist; ST enterotoxin; beta turn mimetic;
 KW gamma-turn mimetic; beta sheet mimetic; disulphide bridge mimetic.
 XX
 XX Escherichia coli.
 XX
 XX WO9909417-A2.
 XX
 XX 25-FEB-1999.
 PD
 XX 20-AUG-1998; 98WO-GB002510.
 PF
 XX 20-AUG-1997; 97GB-00017652.
 PR
 XX (NYCO-) NYCOMED IMAGING AS.
 XX (COCK/) COCKBAIN J.
 XX
 XX Wolfe HR;
 XX
 XX WPI; 1999-181157/15.
 DR
 XX Method of drug selection - using a combination of rational and
 PT combinatorial drug design techniques.
 PT
 XX Disclosure; Page 1-2; 35pp; English.

PS The specification describes a method for selecting a candidate drug
 CC compound having affinity for biological receptors. The method uses a
 CC combination of rational and combinatorial drug design techniques. At
 CC least 1 residue in the original cell receptor binding peptide is modified
 CC to a non-natural amino acid, preferably a beta turn mimetic, a gamma-turn
 CC mimetic, a beta sheet mimetic or a disulphide bridge mimetic. The method
 CC is used for identification of a candidate receptor antagonist or agonist.
 CC The present peptide is a cell receptor binding peptide, and can thus be
 CC used as a starting point for identification of candidate drug compounds,
 CC using the method of the invention
 XX
 XX Sequence 19 AA;

Query Match 95.2%; Score 120; DB 2; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACTGCGY 19
 DB 1 NSSNYCCCLCCNPACTGCGY 19

RESULT 9
 AAY51879
 ID AAY51879 standard; peptide; 19 AA.
 XX
 XX AAY51879;

XX DT 01-FEB-2002 (first entry)
 XX DE Human thermostable enterotoxin Sth peptide fragment #3.
 XX KW Human; thermostable enterotoxin; Sth; metastatic colorectal cancer;
 XX KW guanyl cyclase-C; GC-C; Sth.
 XX OS Homo sapiens.
 XX PN FR2805994-A1.
 XX PD 14-SEP-2001.
 XX PF 10-MAR-2000; 2000FR-00003141.
 XX PR 10-MAR-2000; 2000FR-00003141.
 XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX PI Der Vartanian M, Batisson I;
 XX PS WPI; 2001-640835/74.
 XX PT New compound for detecting and treating metastatic colorectal cancer
 XX PT comprises a conjugate of an Sth peptide and an immunogenic protein which
 XX PT binds to the guanyl cyclase-c receptor.
 XX PS Disclosure; Page 44; 126pp; French.
 XX CC The present invention relates to a conjugate which comprises an E. coli
 XX CC thermostable enterotoxin (Sth) peptide and an active molecule where the
 XX CC Sth peptide has a conjugation such that it is capable of binding to the
 XX CC guanyl cyclase-C (GC-C) receptor. This can be used in the specific
 XX CC diagnosis and treatment of metastatic colorectal cancer. The present
 XX CC sequence is a fragment of the human thermostable enterotoxin (Sth)
 XX CC protein
 XX SQ Sequence 19 AA;
 Query Match 95.2%; Score 120; DB 4; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NSSNYCCCLCCNPACNGCY 19
 Db 1 NSSNYCCCLCCNPACTGCG 19
 |||||
 RESULT 10
 ID AAO16204 standard; peptide; 19 AA.
 XX AC AAO16204;
 XX DT 28-MAR-2003 (first entry)
 XX DE E coli small heat stable enterotoxin tricyclo peptide, SEQ ID No 23.
 XX KW Guanylate cyclase receptor agonist; apoptosis induction; cancer; polyps;
 XX KW inflammation; asthma; nephritis; hepatitis; bronchitis; cystic fibrosis;
 XX KW small heat stable enterotoxin tricyclo; inflammatory bowel disease;
 XX KW pancreatitis; ulcerative colitis; Crohn's disease; Kaposi's sarcoma.
 XX OS Escherichia coli.
 XX PN WO200278683-A1.
 XX FH Key Location/Qualifiers
 XX FT Disulfide-bond 6..10
 XX FT Disulfide-bond 7..15
 XX FT Disulfide-bond 11..18
 XX PN WO200278683-A1.
 XX

PD 10-OCT-2002.
 XX 28-MAR-2002; 2002WO-US009551.
 XX 29-MAR-2001; 2001US-0279437P.
 XX 29-MAR-2001; 2001US-0279438P.
 XX 27-JUN-2001; 2001US-0300850P.
 XX 10-JUL-2001; 2001US-0303806P.
 XX 25-JUL-2001; 2001US-0307358P.
 XX 17-JAN-2002; 2002US-0348646P.
 XX (SYNE-) SYNERGY PHARM INC.
 XX Shailubhai K, Nikiforovich G, Jacob GS;
 XX WPI; 2003-148251/14.
 XX PT Novel guanylate cyclase receptor agonist peptide useful for preventing or
 XX PT treating primary or metastatic cancer and polyps in a patient, and for
 XX PT inducing apoptosis in the cells of a subject.
 XX PS Disclosure; Page 10; 47pp; English.
 XX CC The invention comprises guanylate cyclase receptor agonist peptides that
 XX CC are useful for inducing apoptosis in the cells of a subject. The peptides
 XX CC of the invention may be used to treat: cancer; polyps; inflammation;
 XX CC asthma; nephritis; hepatitis; pancreatitis; bronchitis; cystic fibrosis;
 XX CC inflammatory bowel disease; ulcerative colitis; Crohn's disease; and
 XX CC Kaposi's sarcoma. The present amino acid sequence represents an
 XX CC Escherichia coli small heat stable enterotoxin tricyclo peptide which was
 XX CC used in the invention
 XX SQ Sequence 19 AA;
 Query Match 95.2%; Score 120; DB 6; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NSSNYCCCLCCNPACNGCY 19
 Db 1 NSSNYCCCLCCNPACTGCG 19
 |||||
 RESULT 11
 ID ABG74825 standard; peptide; 19 AA.
 XX AC ABG74825;
 XX DT 12-JUN-2003 (first entry)
 XX DE E. coli heat stable enterotoxin derived peptide SEQ ID 7.
 XX KW Apical membrane; mucosal epithelial cell; respiratory tract;
 XX KW guanylate cyclase C; G protein-coupled receptor; guanosine triphosphate;
 XX KW cyclic guanosine monophosphate; cGMP; chloride ion secretion; inhalation;
 XX KW membrane-associated type II protein kinase; mucus fluidisation;
 XX KW cystic fibrosis transmembrane conductance regulator; breathing disorder;
 XX KW mucus secretion; antiasthmatic; antiinflammatory; bronchial asthma;
 XX KW chronic bronchitis; cystic fibrosis; enterotoxin; heat stable.
 XX OS Escherichia coli.
 XX PN WO200298912-A2.
 XX PD 12-DEC-2002.
 XX PF 05-JUN-2002; 2002WO-DE002040.
 XX PR 05-JUN-2001; 2001DE-01027119.
 XX (CETI/) CETIN Y.
 XX (SAVA/) SAVAS Y.
 XX PA

XX PI Cetin Y, Savas Y;
 XX DR WPI; 2003-156842/15.
 XX
 XX Composition useful for treating respiratory disease, comprises a peptide
 PT that activates guanylate cyclase C, and is delivered to the apical
 PT membrane through the respiratory tract.
 XX
 XX Claim 3; Page 4; 23pp; German.
 XX
 XX This invention describes a novel medicament in a formulation that is
 CC delivered to the apical membrane of mucosal epithelial cells through the
 CC respiratory tract. The medicament contains at least one peptide that
 CC activates guanylate cyclase C (GCC). GCC is a G protein-coupled receptor
 CC that catalyses conversion of guanosine triphosphate to cyclic guanosine
 CC monophosphate (cGMP) and is present on the apical (air) side of
 CC respiratory epithelial cells but not on the basolateral (blood) side.
 CC cGMP activates membrane-associated type II protein kinase which in turn
 CC activates the regulatory domain of the cystic fibrosis transmembrane
 CC conductance regulator, resulting in secretion of chloride ions and water
 CC from the cells, causing fluidisation of the mucus. The products of the
 CC invention are used to make an inhalation device containing the medicament
 CC for diagnosing diseases that are accompanied by breathing disorders or
 CC disorders of mucus secretion in the respiratory tract, by detecting at
 CC least one GCC activator. The products of the invention have antiasthmatic
 CC and antiinflammatory activity. The method is useful for diagnosing and
 CC treating diseases accompanied by breathing disorders or disorders of
 CC mucus secretion in the respiratory tract particularly bronchial asthma,
 CC chronic bronchitis and cystic fibrosis. The product of the invention
 CC improves fluidity and evacuation of bronchial mucus and acts locally
 CC (since the medicament does not enter the bloodstream), so systemic side
 CC effects are minimised. Only very small doses of the medicament are
 CC required. This sequence represents a heat stable E. coli enterotoxin
 CC derived peptide use in an assay to determine guanylate cyclase C
 CC activation described in the disclosure of the invention
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 95.2%; Score 120; DB 6; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 NSSNYCCCLCCNPACNGCY 19
 DB 1 NSSNYCCCLCCNPACTGCGY 19
 RESULT 12
 ADCL4120
 ID ADC14120 standard; peptide; 19 AA.
 XX
 XX ADC14120;
 AC
 XX 18-DEC-2003 (first entry)
 DT
 XX Heat stable enterotoxin, STH.
 DE
 XX Breast cancer; prostate cancer; pancreatic cancer; melanoma;
 KW heat stable enterotoxin; ST motif; tail region; receptor binding region;
 KW cytostatic.
 KW
 XX Escherichia coli.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 6..11
 FT Disulfide-bond 7..15
 FT Disulfide-bond 10..18
 XX
 XX WO2003072125-A1.
 PN
 XX 04-SEP-2003.
 PD
 XX

PF 21-FEB-2003; 2003WO-US005343.
 XX
 XX 22-FEB-2002; 2002US-0359204P.
 XX
 XX (UMOR) UNIV MISSOURI.
 PA
 XX Sieckman G, Gali H, Volkert W, Forte L, Hoffman T;
 PI
 XX WPI; 2003-731571/69.
 DR
 XX
 XX Method of treating or preventing breast, prostate, pancreatic cancer or
 PT melanoma, comprises targeting peptide agent complex to breast cancer
 PT cell, prostate cancer cell, pancreatic cancer cell or melanoma cancer
 PT cell.
 XX
 XX Disclosure; Fig 1; 41pp; English.
 PS
 XX The present invention relates to a method for targeting an agent to a
 CC breast cancer cell, prostate cancer cell, a pancreatic cancer cell or
 CC melanoma cancer cell. The method involves contacting the cancer cell with
 CC a peptide agent complex wherein the peptide comprises an E. coli heat
 CC stable enterotoxin (ST) motif that binds to the cancer cell. The ST motif
 CC may comprise a tail region (ADC14118) and an receptor binding region
 CC (ADCL4119). The method is used for targeting an agent to breast,
 CC prostate, pancreatic or melanoma cancer cell, for rendering, treating and
 CC preventing an unresectable breast, prostate, pancreatic or melanoma
 CC tumour and for identifying tumour binding peptide. The present sequence
 CC is heat stable enterotoxin (STh) produced by human strain of Escherichia
 CC coli bacteria.
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 95.2%; Score 120; DB 7; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 NSSNYCCCLCCNPACNGCY 19
 DB 1 NSSNYCCCLCCNPACTGCGY 19
 RESULT 13
 ADR48340
 ID ADR48340 standard; peptide; 19 AA.
 XX
 XX ADR48340;
 AC
 XX 04-NOV-2004 (first entry)
 DT
 XX Bacterial ST peptide #1.
 DE
 XX Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
 KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; auditory; antileptic; antiasthmatic;
 KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
 KW antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
 KW guanylate cyclase C; GC-C, receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.
 XX
 XX Escherichia coli.
 OS
 XX WO2004069165-A2.
 FN
 XX 19-AUG-2004.
 PD
 XX 28-JAN-2004; 2004WO-US002390.
 PF
 XX

PR 28-JAN-2003; 2003US-0443098P.
 PR 15-MAY-2003; 2003US-0471288P.
 PR 12-NOV-2003; 2003US-0519460P.
 XX (MICR-) MICROBIA INC.
 XX Currie MG, Mahajan-Miklos S;
 XX WPI; 2004-604332/58.
 XX Novel purified peptide capable of activating the guanylate cyclase C
 PT receptor, useful for treating obesity, congestive heart failure and
 PT benign prostatic hyperplasia.
 XX Disclosure; Page 29; 93pp; English.
 XX The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasised or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.
 XX Sequence 19 AA;
 SQ
 Query Match 95.2%; Score 120; DB 8; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 NSSNYCCELCCNPACNGCY 19
 Db 1 NSSNYCCELCCNPACTGCT 19
 RESULT 14
 ADRA48359
 ID ADRA48359 standard; peptide; 19 AA.
 XX
 AC ADRA48359;
 AC
 DT 04-NOV-2004 (first entry)
 XX
 DE Analgesic peptide #2.

XX Gastrointestinal; antiinflammatory; laxative; cardiac; antiulcer;
 KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic;
 KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
 KW antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
 KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.
 XX Unidentified.
 OS
 XX WO2004069165-A2.
 PN
 XX 19-AUG-2004.
 PD
 XX 28-JAN-2004; 2004WO-US002390.
 PF
 XX 28-JAN-2003; 2003US-0443098P.
 PR 15-MAY-2003; 2003US-0471288P.
 PR 12-NOV-2003; 2003US-0519460P.
 XX (MICR-) MICROBIA INC.
 PA Currie MG, Mahajan-Miklos S;
 XX WPI; 2004-604332/58.
 DR Novel purified peptide capable of activating the guanylate cyclase C
 XX receptor, useful for treating obesity, congestive heart failure and
 XX benign prostatic hyperplasia.
 PT Claim 20; Page 61; 93pp; English.
 XX The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel
 CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasised or local colorectal cancer. The current sequence
 CC represents a bacterial ST peptide which is an activator of the GC-C
 CC receptor. ST peptides are considered super agonists of GC-C and are very
 CC resistant to proteolytic degradation.

CC composition of the invention for the treatment of gastrointestinal
 CC disorders.
 XX
 SQ Sequence 19 AA;

Query Match 95.2%; Score 120; DB 8; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
 |||||
 Db 1 NSSNYCCCLCCNPACTGCG 19
 |||||

RESULT 15
 IDR48398
 ID ADR48398 standard; peptide; 19 AA.
 XX
 AC ADR48398;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Peptide used in the creation of a wild-type ST peptide.
 XX
 KW Gastrointestinal; antiinflammatory; laxative; cardiant; antiulcer;
 KW anorectic; cardiovascular; cytostatic; analgesic; CNS; respiratory;
 KW neuroprotective; vasotropic; auditory; antiemetic; antiasthmatic;
 KW nephrotropic; hepatotropic; virucide; immunosuppressive; antiallergic;
 KW antidiabetic; ophthalmological; tranquiliser; hypnotic; nootropic;
 KW guanylate cyclase C; GC-C; receptor; gastrointestinal disorder;
 KW irritable bowel syndrome; constipation; gastroesophageal reflux disease;
 KW heartburn; dyspepsia; gastroparesis; Crohn's disease; ulcerative colitis;
 KW inflammatory bowel disease; obesity; heart failure; cystic fibrosis;
 KW cancer; respiratory disorder; neurological disorder; carbonate imbalance;
 KW erectile dysfunction; inner ear disorder; slow digestion; nausea;
 KW vomiting; bloating; asthma; nephritis; hepatitis; pancreatitis; allergy;
 KW retinopathy; nephropathy; headache; anxiety; sleep disorder.
 XX
 OS Unidentified.
 XX
 XX WO2004069165-A2.
 PN
 XX
 PD 19-AUG-2004.
 XX
 XX 28-JAN-2004; 2004WO-US002390.
 XX
 XX 28-JAN-2003; 2003US-0443098P.
 PR
 XX 15-MAY-2003; 2003US-0471288P.
 PR
 XX 12-NOV-2003; 2003US-0519460P.
 XX
 XX (MICR-) MICROBIA INC.
 PA
 XX
 XX Currie MG, Mahajan-Miklos S;
 PI
 XX
 XX WPI; 2004-604332/58.
 DR
 XX
 XX Novel purified peptide capable of activating the guanylate cyclase C
 PT receptor, useful for treating obesity, congestive heart failure and
 PT benign prostatic hyperplasia.
 PT
 XX
 XX Example 1; Page 39; 93pp; English.
 PS
 XX
 CC The invention relates to a purified peptide (P1) capable of activating
 CC the guanylate cyclase C (GC-C) receptor. Further disclosed is a
 CC pharmaceutical composition comprising the peptide of the invention. The
 CC composition of the invention is useful for treating a gastrointestinal
 CC disorder in a patient, which involves administering P1, where the
 CC gastrointestinal disorder is gastrointestinal motility disorder,
 CC irritable bowel syndrome, chronic constipation, a functional
 CC gastrointestinal disorder, gastroesophageal reflux disease, functional
 CC heartburn, dyspepsia, functional dyspepsia, nonulcer dyspepsia,
 CC gastroparesis, chronic intestinal pseudo-obstruction, colonic pseudo-
 CC obstruction, Crohn's disease, ulcerative colitis or inflammatory bowel

CC disease. The peptide of the invention is also useful for treating
 CC obesity, congestive heart failure, cystic fibrosis or a patient suffering
 CC from constipation. The P1/GC-C receptor agonist is useful for treating
 CC cancer, respiratory disorder, neurological disorder, disorder associated
 CC with carbonate imbalance, erectile dysfunction, insulin-related disorder
 CC or inner ear disorder. P1 is useful in treating slow digestion or slow
 CC stomach emptying. P1 is useful in relieving symptoms of gastroparesis
 CC such as nausea, vomiting, bloating, and delayed gastric emptying. P1 is
 CC useful for treating or preventing asthma, nephritis, hepatitis,
 CC pancreatitis, allergies, etc. P1 is useful for treating or preventing
 CC type II diabetes mellitus, hyperglycaemia, respiratory disorders
 CC including inhalation. P1 is useful in treating or preventing retinopathy,
 CC nephropathy and edema formation. P1 is useful for treating or preventing
 CC headache, anxiety, sleep disorders and memory loss. P1 is useful as a
 CC marker to identify, detect, stage, or diagnosis diseases and conditions
 CC of the small intestine, including Crohn's disease, colitis, inflammatory
 CC bowel disease, tumours, etc. P1 can be conjugated to diagnostic or
 CC therapeutic molecule to target cells bearing GC-C receptor, e.g., cystic
 CC fibrosis lesions and specific cells lining the intestinal tract, thus
 CC useful in targeting radioactive moieties or therapeutic moieties to the
 CC intestine to aid in imaging and diagnosing or treating
 CC colorectal/metastasised or local colorectal cancer. The current sequence
 CC represents an peptide used in an example from the invention in the
 CC preparation of variant ST peptides and wild-type ST peptide.

XX Sequence 19 AA;

Query Match 95.2%; Score 120; DB 8; Length 19;
 Best Local Similarity 94.7%; Pred. No. 9.1e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19

Db 1 NSSNYCCCLCCNPACTGCG 19

Search completed: March 26, 2005, 16:44:27
 Job time : 20.8029 secs

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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:38:19 ; Search time 5.68613 Seconds
(without alignments)
249.437 Million cell updates/sec

Title: US-10-775-481A-5
Perfect score: 126
Sequence: 1 NSSNYCCELCCNPACNGCY 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	19	1 US-08-141-892A-5	Sequence 5, Appli
2	126	100.0	19	2 US-08-583-447A-5	Sequence 5, Appli
3	126	100.0	19	2 US-08-467-920-5	Sequence 5, Appli
4	126	100.0	19	3 US-08-635-930-5	Sequence 5, Appli
5	126	100.0	19	3 US-09-193-997-5	Sequence 5, Appli
6	126	100.0	19	3 US-09-138-237A-5	Sequence 5, Appli
7	114	90.5	18	1 US-08-141-892A-33	Sequence 33, Appl
8	114	90.5	18	2 US-08-583-447A-33	Sequence 33, Appl
9	114	90.5	18	2 US-08-467-920-33	Sequence 33, Appl
10	114	90.5	18	3 US-08-635-930-33	Sequence 33, Appl
11	114	90.5	18	3 US-09-193-997-33	Sequence 33, Appl
12	114	90.5	18	3 US-09-138-237A-33	Sequence 33, Appl
13	113	89.7	18	1 US-08-141-892A-27	Sequence 27, Appl
14	113	89.7	18	2 US-08-583-447A-27	Sequence 27, Appl
15	113	89.7	18	2 US-08-467-920-27	Sequence 27, Appl
16	113	89.7	18	3 US-08-635-930-27	Sequence 27, Appl
17	113	89.7	18	3 US-09-193-997-27	Sequence 27, Appl
18	113	89.7	18	3 US-09-138-237A-27	Sequence 27, Appl
19	112	88.9	19	1 US-08-141-892A-49	Sequence 49, Appl
20	112	88.9	19	2 US-08-583-447A-49	Sequence 49, Appl
21	112	88.9	19	2 US-08-467-920-49	Sequence 49, Appl
22	112	88.9	19	3 US-08-635-930-49	Sequence 49, Appl
23	112	88.9	19	3 US-09-193-997-49	Sequence 49, Appl
24	112	88.9	19	3 US-09-138-237A-49	Sequence 49, Appl
25	110	87.3	17	1 US-08-141-892A-34	Sequence 34, Appl
26	110	87.3	17	2 US-08-583-447A-34	Sequence 34, Appl
27	110	87.3	17	2 US-08-467-920-34	Sequence 34, Appl

28	110	87.3	17	3 US-08-635-930-34	Sequence 34, Appl
29	110	87.3	17	3 US-09-193-997-34	Sequence 34, Appl
30	110	87.3	17	3 US-09-138-237A-34	Sequence 34, Appl
31	107	84.9	17	1 US-08-141-892A-28	Sequence 28, Appl
32	107	84.9	17	2 US-08-583-447A-28	Sequence 28, Appl
33	107	84.9	17	2 US-08-467-920-28	Sequence 28, Appl
34	107	84.9	17	3 US-08-635-930-28	Sequence 28, Appl
35	107	84.9	17	3 US-09-193-997-28	Sequence 28, Appl
36	107	84.9	17	3 US-09-138-237A-28	Sequence 28, Appl
37	106	84.1	16	1 US-08-141-892A-35	Sequence 35, Appl
38	106	84.1	16	2 US-08-583-447A-35	Sequence 35, Appl
39	106	84.1	16	2 US-08-467-920-35	Sequence 35, Appl
40	106	84.1	16	3 US-08-635-930-35	Sequence 35, Appl
41	106	84.1	16	3 US-09-193-997-35	Sequence 35, Appl
42	106	84.1	16	3 US-09-138-237A-35	Sequence 35, Appl
43	103	81.7	16	1 US-08-141-892A-29	Sequence 29, Appl
44	103	81.7	16	2 US-08-583-447A-29	Sequence 29, Appl
45	103	81.7	16	2 US-08-467-920-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-141-892A-5
; Sequence 5, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: Of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-141-892A-5

Query Match 100.0%; Score 126; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACNGCY 19

```
RESULT 2
US-08-583-447A-5
; Sequence 5, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-583-447A-5
Query Match 100.0%; Score 126; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 3
US-08-467-920-5
; Sequence 5, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5962220ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-920-5
Query Match 100.0%; Score 126; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 4
US-08-635-930-5
; Sequence 5, Application US/08635930
; Patent No. 6060037
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-635-930-5

Query Match 100.0%; Score 126; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACNGCY 19

RESULT 5
US-09-193-997-5
Sequence 5, Application US/09193997
Patent No. 6087109
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically Bind To Colorectal Cancer Cells
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,997
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,920
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-193-997-5

Query Match 100.0%; Score 126; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCELCCNPACNGCY 19

Db 1 NSSNYCCELCCNPACNGCY 19

RESULT 6
US-09-138-237A-5
Sequence 5, Application US/09138237A
Patent No. 6268159
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,237A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-138-237A-5

Query Match 100.0%; Score 126; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACNGCY 19

RESULT 7
US-08-141-892A-33
Sequence 33, Application US/08141892A
Patent No. 5518888
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: Of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5 inch disk, 720 Kb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/141,892A
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-0903
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-141-892A-33

Query Match 90.5%; Score 114; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 8.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy~ 2 SSNYCCCLCCNPACNGCY 19
Db 1 SSNYCCCLCCNPACTGCT 18

RESULT 8
US-08-583-447A-33
; Sequence 33, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 58796566ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-583-447A-33

Query Match 90.5%; Score 114; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 8.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SSNYCCCLCCNPACNGCY 19
Db 1 SSNYCCCLCCNPACTGCT 18

RESULT 9
US-08-467-920-33
; Sequence 33, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind to Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5962220ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-467-920-33

Query Match 90.5%; Score 114; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 8.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SSNYCCCLCCNPACNGCY 19
Db 1 SSNYCCCLCCNPACTGCT 18

RESULT 10
US-08-635-930-33
; Sequence 33, Application US/08635930

Patent No. 6060037
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically Bind To
; TITLE OF INVENTION: Colorectal Cancer Cells And Methods Of Using
; TITLE OF INVENTION: The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6060037ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WordPerfect 6.0/6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,930
; FILING DATE: 26-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,056
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-635-930-33

Query Match 90.5%; Score 114; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 8.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSNYCCCLCCNPACNGCY 19
Db 1 SSNYCCCLCCNPACTGCGY 18

RESULT 11
US-09-193-997-33
; Sequence 33, Application US/09193997
; Patent No. 6087109
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSSEE: No. 6087109ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/193,997
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,920
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-193-997-33

Query Match 90.5%; Score 114; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 8.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSNYCCCLCCNPACNGCY 19
Db 1 SSNYCCCLCCNPACTGCGY 18

RESULT 12
US-09-138-237A-33
; Sequence 33, Application US/09138237A
; Patent No. 6268159
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: of Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6268159ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,237A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-138-237A-33

Query Match 90.5%; Score 114; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 8.6e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SSNYCCCLCCNPACNGCY 19
Db 1 SSNYCCCLCCNPACTGCY 18

RESULT 13

US-08-141-892A-27
; Sequence 27, Application US/08141892A
; Patent No. 5518888
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
; TITLE OF INVENTION: OF Using the Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5518888ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,892A
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-141-892A-27

Query Match 89.7%; Score 113; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSNYCCCLCCNPACNGC 18
Db 1 SSNYCCCLCCNPACTGC 18

RESULT 14

US-08-583-447A-27
; Sequence 27, Application US/08583447A
; Patent No. 5879656
; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; TITLE OF INVENTION: Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5879656ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,447A
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-583-447A-27

Query Match 89.7%; Score 113; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSNYCCCLCCNPACNGC 18
Db 1 SSNYCCCLCCNPACTGC 18

RESULT 15

US-08-467-920-27
; Sequence 27, Application US/08467920
; Patent No. 5962220
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5962220ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,920

Query Match 89.7%; Score 113; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSNYCCCLCCNPACNGC 18
Db 1 SSNYCCCLCCNPACTGC 18

;; FILING DATE: 435
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/141,892
;; FILING DATE: 26-OCT-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1589
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-467-920-27

Query Match 89.7%; Score 113; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCELCCNPACNGC 18
|||
Db 1 NSSNYCCELCCNPACTGC 18

Search completed: March 26, 2005, 16:51:12
Job time : 5.68613 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:48:40 ; Search time 18.9307 Seconds
(without alignments)
332.314 Million cell updates/sec

Title: US-10-775-481A-5

Perfect score: 126

Sequence: 1 NSSNYCCLCNFACNGCY 19

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	126	100.0	19 15	US-10-621-684-5 Sequence 5, Appli
2	120	95.2	19 14	US-10-107-814-23 Sequence 23, Appli
3	120	95.2	19 15	US-10-371-966-1 Sequence 1, Appli
4	120	95.2	19 17	US-10-796-719-1 Sequence 1, Appli
5	120	95.2	19 17	US-10-796-719-26 Sequence 26, Appli
6	120	95.2	19 17	US-10-479-606-7 Sequence 7, Appli
7	120	95.2	21 17	US-10-796-719-39 Sequence 39, Appli
8	120	95.2	21 17	US-10-796-719-21 Sequence 21, Appli
9	118	93.7	19 17	US-10-796-719-84 Sequence 84, Appli
10	118	93.7	19 17	US-10-796-719-86 Sequence 86, Appli
11	117	92.9	19 17	US-10-796-719-92 Sequence 92, Appli
12	116	92.1	19 15	US-10-371-966-2 Sequence 2, Appli
13	116	92.1	19 17	US-10-796-719-27 Sequence 27, Appli

14	116	92.1	19 17	US-10-796-719-87	Sequence 87, Appl
15	116	92.1	21 17	US-10-796-719-40	Sequence 40, Appl
16	116	92.1	21 17	US-10-796-719-41	Sequence 41, Appl
17	115	91.3	19 17	US-10-796-719-28	Sequence 28, Appl
18	115	91.3	19 17	US-10-796-719-75	Sequence 75, Appl
19	115	91.3	19 17	US-10-796-719-79	Sequence 79, Appl
20	115	91.3	19 17	US-10-796-719-90	Sequence 90, Appl
21	115	91.3	21 17	US-10-796-719-42	Sequence 42, Appl
22	114	90.5	18 15	US-10-621-684-33	Sequence 33, Appl
23	114	90.5	19 17	US-10-796-719-76	Sequence 76, Appl
24	114	90.5	19 17	US-10-796-719-80	Sequence 80, Appl
25	114	90.5	19 17	US-10-796-719-85	Sequence 85, Appl
26	114	90.5	19 17	US-10-796-719-89	Sequence 89, Appl
27	114	90.5	21 17	US-10-796-719-91	Sequence 91, Appl
28	114	90.5	21 17	US-10-796-719-43	Sequence 43, Appl
29	114	90.5	21 17	US-10-796-719-44	Sequence 44, Appl
30	114	90.5	21 17	US-10-796-719-45	Sequence 45, Appl
31	113	89.7	18 15	US-10-621-684-27	Sequence 27, Appl
32	113	89.7	19 17	US-10-796-719-77	Sequence 77, Appl
33	113	89.7	19 17	US-10-796-719-81	Sequence 81, Appl
34	113	89.7	19 17	US-10-796-719-83	Sequence 83, Appl
35	113	89.7	19 17	US-10-796-719-88	Sequence 88, Appl
36	112	88.9	19 15	US-10-621-684-49	Sequence 49, Appl
37	112	88.9	19 17	US-10-796-719-68	Sequence 68, Appl
38	112	88.9	19 17	US-10-796-719-78	Sequence 78, Appl
39	112	88.9	19 17	US-10-796-719-82	Sequence 82, Appl
40	110	87.3	17 15	US-10-621-684-34	Sequence 34, Appl
41	109	86.5	18 17	US-10-796-719-72	Sequence 72, Appl
42	109	86.5	19 17	US-10-796-719-67	Sequence 67, Appl
43	109	86.5	19 17	US-10-796-719-69	Sequence 69, Appl
44	109	86.5	19 17	US-10-796-719-70	Sequence 70, Appl
45	109	86.5	19 17	US-10-796-719-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1

US-10-621-684-5

Sequence 5, Application US/10621684

Publication No. US20040029182A1

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

TITLE OF INVENTION: ST Receptor Binding Compounds and

Methods of Using the Same

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20040029182A1ris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/621,684

FILING DATE: 17-Jul-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/583,447A

FILING DATE: 05-JAN-1996

APPLICATION NUMBER: US 08/141,892

FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1702

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-621-684-5

Query Match 100.0%; Score 126; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACNGCY 19

RESULT 2

US-10-107-814-23
; Sequence 23, Application US/10107814
; Publication No. US20030073628A1
; GENERAL INFORMATION:
; APPLICANT: SHAILUBHAI, KUNWAR
; APPLICANT: NIKIFOROVICH, GREGORY
; APPLICANT: JACOB, GARY S.
; TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
; OF TISSUE INFLAMMATION AND CARCINOGENESIS
; FILE REFERENCE: 81361/284943/WAS
; CURRENT APPLICATION NUMBER: US/10/107,814
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (6)..(10)
; NAME/KEY: DISULFID
; LOCATION: (7)..(15)
; NAME/KEY: DISULFID
; LOCATION: (11)..(18)
US-10-107-814-23

Query Match 95.2%; Score 120; DB 14; Length 19;
Best Local Similarity 94.7%; Pred. No. 8.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACTGCY 19

RESULT 3

US-10-371-966-1
; Sequence 1, Application US/10371966
; Publication No. US20030232013A1
; GENERAL INFORMATION:
; APPLICANT: SIECKMAN, GARY
; APPLICANT: VOLKERT, WYNN
; APPLICANT: FORTE, LEONARD
; APPLICANT: HOFFMAN, TIMOTHY
; APPLICANT: GALLI, HARIPRASAD
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TARGETING OF CANCERS CELLS
; FILE REFERENCE: UWMO:013US
; CURRENT APPLICATION NUMBER: US/10/371,966
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/359,204
; PRIOR FILING DATE: 2002-02-22

; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-371-966-1

Query Match 95.2%; Score 120; DB 15; Length 19;
Best Local Similarity 94.7%; Pred. No. 8.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACTGCY 19

RESULT 4

US-10-796-719-1
; Sequence 1, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-1

Query Match 95.2%; Score 120; DB 17; Length 19;
Best Local Similarity 94.7%; Pred. No. 8.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
Db 1 NSSNYCCCLCCNPACTGCY 19

RESULT 5

US-10-796-719-26
; Sequence 26, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-26

Query Match 95.2%; Score 120; DB 17; Length 19;
Best Local Similarity 94.7%; Pred. No. 8.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACTGCT 19
|||||

RESULT 6
US-10-479-606-7
; Sequence 7, Application US/10479606
; Publication No. US20050032684A1
; GENERAL INFORMATION:
; APPLICANT: Cetin, Yalcin
; APPLICANT: Savas, Yuxsel
; TITLE OF INVENTION: Guanylate-cyclase C ligand, administered via the airways, for the
; TITLE OF INVENTION: treatment of respiratory airway problems
; FILE REFERENCE: 03100192aa
; CURRENT APPLICATION NUMBER: US/10/479,606
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: DE10127119.0
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/DE02/02040
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: escherichia coli
US-10-479-606-7

Query Match 95.2%; Score 120; DB 17; Length 19;
Best Local Similarity 94.7%; Pred. No. 8.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACTGCT 19
|||||

RESULT 7
US-10-796-719-39
; Sequence 39, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288

; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-39

Query Match 95.2%; Score 120; DB 17; Length 21;
Best Local Similarity 94.7%; Pred. No. 9.1e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCELCCNPACNGCY 19
Db 1 NSSNYCCELCCNPACTGCT 19
|||||

RESULT 8
US-10-796-719-21
; Sequence 21, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-796-719-21

Query Match 95.2%; Score 120; DB 17; Length 72;
Best Local Similarity 94.7%; Pred. No. 2.4e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCELCCNPACNGCY 19
Db 54 NSSNYCCELCCNPACTGCT 72
|||||

RESULT 9
US-10-796-719-84
; Sequence 84, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28

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; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-84

Query Match          93.7%; Score 118; DB 17; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.4e-06;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
Db      1 NSSNYCCCLCCNPACTGCG 19

RESULT 10
US-10-796-719-86
; Sequence 86, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-86

Query Match          93.7%; Score 118; DB 17; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.4e-06;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
Db      1 NSSNYCCCLCCNPACTGCG 19

RESULT 11
US-10-796-719-92
; Sequence 92, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
; APPLICANT: Mahajan-Miklos, Shalina
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
; FILE REFERENCE: 14184-043001
; CURRENT APPLICATION NUMBER: US/10/796,719
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US 10/766,735
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/443,098
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/471,288
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/519,460
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-86

Query Match          93.7%; Score 118; DB 17; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.4e-06;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
Db      1 NSSNYCCCLCCNPACTGCG 19

RESULT 12
US-10-371-966-2
; Sequence 2, Application US/10371966
; Publication No. US20030232013A1
; GENERAL INFORMATION:
; APPLICANT: SIECKMAN, GARY
; APPLICANT: VOLKERT, WYNN
; APPLICANT: FORTE, LEONARD
; APPLICANT: HOFFMAN, TIMOTHY
; APPLICANT: GALLI, HARIPRASAD
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TARGETING OF CANCERS CELLS
; TITLE OF INVENTION: WITH TUMOR HOMING PEPTIDES
; FILE REFERENCE: UVMO:013US
; CURRENT APPLICATION NUMBER: US/10/371,966
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/359,204
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-371-966-2

Query Match          92.1%; Score 116; DB 15; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e-06;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NSSNYCCCLCCNPACNGCY 19
Db      1 NSSNYCCCLCCNPACTGCG 19

RESULT 13
US-10-796-719-27
; Sequence 27, Application US/10796719
; Publication No. US20050020811A1
; GENERAL INFORMATION:
; APPLICANT: Currie, Mark G.
```

;; APPLICANT: Mahajan-Miklos, Shalina
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
;; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
;; FILE REFERENCE: 14184-043001
;; CURRENT APPLICATION NUMBER: US/10/796,719
;; CURRENT FILING DATE: 2004-03-09
;; PRIOR APPLICATION NUMBER: US 10/766,735
;; PRIOR FILING DATE: 2004-01-28
;; PRIOR APPLICATION NUMBER: US 60/443,098
;; PRIOR FILING DATE: 2003-01-28
;; PRIOR APPLICATION NUMBER: US 60/471,288
;; PRIOR FILING DATE: 2003-05-15
;; PRIOR APPLICATION NUMBER: US 60/519,460
;; PRIOR FILING DATE: 2003-11-12
;; NUMBER OF SEQ ID NOS: 149
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 27
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-27

Query Match 92.1%; Score 116; DB 17; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.3e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACGCGY 19
Db 1 NSSNYCCCLCCNPACGCGY 19

RESULT 14

US-10-796-719-87
;; Sequence 87, Application US/10796719
;; Publication No. US20050020811A1
;; GENERAL INFORMATION:
;; APPLICANT: Currie, Mark G.
;; APPLICANT: Mahajan-Miklos, Shalina
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
;; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
;; FILE REFERENCE: 14184-043001
;; CURRENT APPLICATION NUMBER: US/10/796,719
;; CURRENT FILING DATE: 2004-03-09
;; PRIOR APPLICATION NUMBER: US 10/766,735
;; PRIOR FILING DATE: 2004-01-28
;; PRIOR APPLICATION NUMBER: US 60/443,098
;; PRIOR FILING DATE: 2003-01-28
;; PRIOR APPLICATION NUMBER: US 60/471,288
;; PRIOR FILING DATE: 2003-05-15
;; PRIOR APPLICATION NUMBER: US 60/519,460
;; PRIOR FILING DATE: 2003-11-12
;; NUMBER OF SEQ ID NOS: 149
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 87
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-87

Query Match 92.1%; Score 116; DB 17; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACGCGY 19
Db 1 NSSNYCCCLCCNPACGCGY 19

RESULT 15

US-10-796-719-40
;; Sequence 40, Application US/10796719
;; Publication No. US20050020811A1
;; GENERAL INFORMATION:
;; APPLICANT: Currie, Mark G.
;; APPLICANT: Mahajan-Miklos, Shalina
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
;; TITLE OF INVENTION: TREATMENT OF GASTROINTESTINAL DISORDERS
;; FILE REFERENCE: 14184-043001
;; CURRENT APPLICATION NUMBER: US/10/796,719
;; CURRENT FILING DATE: 2004-03-09
;; PRIOR APPLICATION NUMBER: US 10/766,735
;; PRIOR FILING DATE: 2004-01-28
;; PRIOR APPLICATION NUMBER: US 60/443,098
;; PRIOR FILING DATE: 2003-01-28
;; PRIOR APPLICATION NUMBER: US 60/471,288
;; PRIOR FILING DATE: 2003-05-15
;; PRIOR APPLICATION NUMBER: US 60/519,460
;; PRIOR FILING DATE: 2003-11-12
;; NUMBER OF SEQ ID NOS: 149
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 40
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide
US-10-796-719-40

Query Match 92.1%; Score 116; DB 17; Length 21;
Best Local Similarity 94.7%; Pred. No. 2.5e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACGCGY 19
Db 1 NSSNYCCCLCCNPACGCGY 19

Search completed: March 26, 2005, 17:16:37
Job time : 18.9307 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:49 ; Search time 4.0219 Seconds
(without alignments)
454.541 Million cell updates/sec

Title: US-10-775-481A-5
Perfect score: 126
Sequence: 1 NSSNYCCCLCCNPACNGCY 19
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	95.2	72	1 QHEC4	heat-stable entero
2	120	95.2	72	1 QHEC1B	heat-stable entero
3	103	81.7	72	1 QHEC1	heat-stable entero
4	98	77.8	18	2 A60103	heat-stable entero
5	89	70.6	53	2 S88705	heat-stable entero
6	88	69.8	66	2 S31652	enterotoxin - Yers
7	83	65.9	18	1 QHEC2	heat-stable entero
8	81	64.3	17	2 A54534	heat-stable entero
9	81	64.3	78	1 QHVC1	heat-stable entero
10	78.5	62.3	71	2 S25659	heat-stable entero
11	69	54.8	65	2 S34671	heat-stable entero
12	62.5	49.6	186	2 A45910	ultra-high-sulfur
13	59	46.8	112	2 JC4651	uroguanylin precu
14	58	46.0	116	2 JC7620	guanylin precursor
15	54.5	43.3	122	2 JC6548	high sulfur protei
16	54.5	43.3	369	2 T24022	hypothetical prote
17	54	42.9	56	1 W7FF	testis-specific pr
18	54	42.9	68	2 S25775	testis-specific pr
19	54	42.9	415	2 T19234	hypothetical prote
20	53.5	42.5	64	2 A25775	metallothionein A
21	53.5	42.5	64	2 A33825	metallothionein A
22	53.5	42.5	410	2 T24020	hypothetical prote
23	53	42.1	133	2 T37286	cysteine proteinas
24	53	42.1	172	2 T47108	high-sulfur wool m
25	53	42.1	400	2 T22853	probable cathepsin
26	52.5	41.7	152	2 T18975	hypothetical prote
27	52.5	41.7	164	2 T24272	hypothetical prote
28	52.5	41.7	176	2 T31796	hypothetical prote
29	52.5	41.7	188	2 T15651	hypothetical prote

30 52 41.3 152 1 KRSHHC keratin high-sulfu
31 52 41.3 152 2 I47111 high-sulfur wool m
32 52 41.3 152 2 I47109 high-sulfur wool m
33 52 41.3 152 2 I47108 high-sulfur wool m
34 52 41.3 152 2 I47112 high-sulfur wool m
35 52 41.3 156 1 KRSHHB keratin high-sulfu
36 52 41.3 162 2 I47107 high-sulfur wool m
37 52 41.3 172 1 KRSHHA keratin high-sulfu
38 52 41.3 182 1 KRSHHD keratin high-sulfu
39 52 41.3 182 2 I47105 high-sulfur wool m
40 52 41.3 188 2 JC6547 high sulfur protei
41 52 41.3 1299 2 T43251 furin (EC 3.4.21.7
42 51 40.5 248 2 T19913 hypothetical prote
43 51 40.5 525 2 G71317 hypothetical prote
44 50.5 40.1 72 1 TIZB1P proteinase inhibit
45 50.5 40.1 78 1 TIZB1A proteinase inhibit

ALIGNMENTS

RESULT 1

QHEC4
heat-stable enterotoxin STA4 precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0373; A35978
R:Stieglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.;
Plasmid 20, 42-53, 1988
A:Title: Cloning, sequencing, and expression in ficoll-generated minicells of an Escheri
A:Reference number: JT0373; MUID:89202548; PMID:3071819
A:Accession: JT0373
A:Molecule type: DNA
A:Residues: 1-72 <STI>
A:Cross-references: UNIPROT:P07965; GB:J03311; NID:G147875; PIDN:AAA24652.1; PID:G147876
R:Zhong, X.; Shen, L.P.; Chi, C.W.
Toxicon 28, 453-456, 1990
A:Title: Isolation and nucleotide sequence determination of a gene encoding a heat-stabl
A:Reference number: A35978; MUID:90273381; PMID:2190361
A:Accession: A35978
A:Molecule type: DNA
A:Residues: 1-72 <ZHO>
C:Genetics:
A:Gene: estA4
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-53/Domain: propeptide #status predicted <PRO>
F:54-72/Product: heat-stable enterotoxin #status predicted <MAT>
F:59-64,60-68,63-71/Disulfide bonds: #status predicted

Query Match 95.2% Score 120: DB 1; Length 72;
Best Local Similarity 94.7%; Pred. No. 5.3e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACNGCY 19
|||||
Db 54 NSSNYCCCLCCNPACTGCG 72
|||||

RESULT 2

QHEC1B
heat-stable enterotoxin ST-Ib precursor - Escherichia coli
N:Alternate names: heat-stable enterotoxin ST-A2
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: JS0292; A33068; A30567
R:Moseley, S.L.; Hardy, J.W.; Huq, M.I.; Echeverria, P.; Falkow, S.
Infect. Immun. 39, 1167-1174, 1983
A:Title: Isolation and nucleotide determination of a gene encoding a heat-stable enteroto
A:Reference number: JS0292; MUID:83184648; PMID:6341230
A:Accession: JS0292
A:Molecule type: DNA

A;Residues: 1-72 <MOS>
A;Cross-references: UNIPROT:Q47185; UNIPROT:P07965; GB:M34916; NID:g146407; PIDN:AAA23399
R;Dwarakanath, P.; Vlaswariyah, S.S.; Subrahmanyam, Y.V.B.K.; Shanthi, G.; Jagannatha, Gene 81, 219-226, 1989
A;Title: Cloning and hyperexpression of a gene encoding the heat-stable toxin of *Escherichia coli* serotype O157:H7
A;Reference number: A33068; MUID:90034194; PMID:2680769
A;Accession: A33068
A;Molecule type: DNA
A;Residues: 1-18, 'A', 20-72 <DNA>
A;Cross-references: GB:M29255; NID:g148029; PIDN:AAA24686.1; PID:g148030
A;Note: the authors translated the codon AAG for residue 2 as Val and CTA for residue 34
R;Aimoto, S.; Takao, T.; Shimomishi, Y.; Hara, S.; Takeda, T.; Takeda, Y.; Miwatani, T. Eur. J. Biochem. 129, 257-263, 1992
A;Title: Amino acid sequence of heat-stable enterotoxin produced by human enterotoxigenic *Escherichia coli* serotype O157:H7
A;Reference number: A33067; MUID:83105138; PMID:6759126
A;Accession: A33067
A;Molecule type: protein
A;Residues: 54-72 <AIM>
R;Guzman-Verduzco, L.M.; Kupersztoch, Y.M. Infect. Immun. 57, 645-648, 1989
A;Title: Rectification of two *Escherichia coli* heat-stable enterotoxin allele sequences
A;Reference number: A30567; MUID:89108616; PMID:2643580
A;Accession: A30567
A;Molecule type: DNA
A;Residues: 1-18, 'A', 20-24, 'AG', 27-41, 'V', 43-44, 'N', 46, 'E', 48, 'S', 50-72 <GUZ>
A;Cross-references: GB:M18345; NID:g145862; PIDN:AAA23729.1; PID:g145863
A;Comment: This is one of the type I heat-stable enterotoxins that are methanol-soluble.
C;Genetics:
A;Gene: st
C;Superfamily: heat-stable enterotoxin ST
C;Keywords: enterotoxin; heat-stable protein
F;1-53/Domain: signal sequence and propeptide #status predicted <SIG>
F;54-72/Product: heat-stable enterotoxin ST-Ib #status experimental <WAT>
F;59-64,60-68,63-71/Disulfide bonds: #status experimental

Query Match 95.2%; Score 120; DB 1; Length 72;
Best Local Similarity 94.7%; Pred. No. 5.3e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
DB 54 NSSNYCCCLCCNPACNGCY 72

RESULT 3
QHEC1
heat-stable enterotoxin ST-I precursor - *Escherichia coli*
N;Alternate names: heat-stable enterotoxin estA1
C;Species: *Escherichia coli*
C;Date: 31-Aug-1980 #sequence revision 31-Aug-1980 #text_change 09-Jul-2004
A;Accession: A01822; A30985; A36732; JT0374; I51932
R;So, M.; McCarthy, B.J. Proc. Natl. Acad. Sci. U.S.A. 77, 4011-4015, 1980
A;Title: Nucleotide sequence of the bacterial transposon Tn1681 encoding a heat-stable (S) enterotoxin of *Escherichia coli* serotype O157:H7
A;Reference number: A01822; MUID:81054703; PMID:6254008
A;Accession: A01822
A;Molecule type: DNA
A;Residues: 1-72 <LAZ>
A;Cross-references: UNIPROT:P01559; GB:V00612; GB:J01831; NID:g43704; PIDN:CAA23883.1; F;Lazure, C.; Seidah, N.G.; Chretien, M.; Lallier, R.; St-Pierre, S. Can. J. Biochem. Cell Biol. 61, 287-292, 1983
A;Title: Primary structure determination of *Escherichia coli* heat-stable enterotoxin of serotype O157:H7
A;Reference number: A30985; MUID:83284515; PMID:6349752
A;Accession: A30985
A;Molecule type: protein
A;Residues: 55-72 <LAZ>
A;Experimental source: strain F11
R;Dallas, W.S. J. Bacteriol. 172, 5490-5493, 1990
A;Title: The heat-stable toxin I gene from *Escherichia coli* 18D.
A;Reference number: A36732; MUID:90368614; PMID:2203756
A;Accession: A36732
A;Molecule type: DNA

A;Residues: 1-72 <DAL>
A;Cross-references: GB:M58746; NID:g145860; PIDN:AAA62776.1; PID:g145861
A;Experimental source: strain 18D
R;Stiglitz, H.; Cervantes, L.; Robledo, R.; Fonseca, R.; Covarrubias, L.; Bolivar, F.; Plasmid 20, 42-53, 1988
A;Title: Cloning, sequencing, and expression in *Escherichia coli* heat-stable enterotoxin
A;Reference number: JT0373; MUID:89202548; PMID:3071819
A;Accession: JT0373
A;Molecule type: DNA
A;Residues: 1-72 <STI>
R;Sekizaki, T.; Akashi, H.; Terakado, N. Am. J. Vet. Res. 46, 909-912, 1985
A;Title: Nucleotide sequences of the genes for *Escherichia coli* heat-stable enterotoxin
A;Reference number: I51933; MUID:85249571; PMID:2990268
A;Accession: I51932
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-69, 'P', 71-72 <RES>
A;Cross-references: GB:M25607; NID:g147877; PIDN:AAA24653.1; PID:g147878
C;Comment: Both heat-stable and heat-labile enterotoxins are produced by pathogenic strains of *Escherichia coli*.
C;Superfamily: heat-stable enterotoxin ST
C;Keywords: enterotoxin; heat-stable protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-54/Domain: propeptide #status predicted <PRO>
F;55-72/Product: heat-stable enterotoxin ST-I #status experimental <WAT>
F;59-64,60-68,63-71/Disulfide bonds: #status predicted

Query Match 81.7%; Score 103; DB 1; Length 72;
Best Local Similarity 78.9%; Pred. No. 4e-05;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
DB 54 NNTFYCCCLCCNPACNGCY 72

RESULT 4
A60103
heat-stable enterotoxin ST-Ia - *Citrobacter freundii*
C;Species: *Citrobacter freundii*
C;Date: 10-Nov-1992 #sequence revision 10-Nov-1992 #text_change 09-Jul-2004
A;Accession: A60103
R;Guarino, A.; Giannella, R.; Thompson, M.R. Infect. Immun. 57, 649-652, 1989
A;Title: *Citrobacter freundii* produces an 18-amino-acid heat-stable enterotoxin identical to *Escherichia coli* serotype O157:H7
A;Reference number: A60103; MUID:89108617; PMID:2912902
A;Accession: A60103
A;Molecule type: protein
A;Residues: 1-18 <GUA>
A;Cross-references: UNIPROT:Q7M0U3
C;Superfamily: heat-stable enterotoxin ST

Query Match 77.8%; Score 98; DB 2; Length 18;
Best Local Similarity 93.3%; Pred. No. 6.2e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 YCCCLCCNPACNGCY 19
DB 4 YCCCLCCNPACNGCY 18

RESULT 5
S68705
heat-stable enterotoxin Y-Stc - *Yersinia enterocolitica*
C;Species: *Yersinia enterocolitica*
C;Date: 25-Feb-1998 #sequence revision 13-Mar-1998 #text_change 13-Mar-1998
A;Accession: S68705
R;Yoshino, K.; Takao, T.; Huang, X.; Murata, H.; Nakao, H.; Takeda, T.; Shimomishi, Y. PNAS Lett. 362, 319-322, 1995
A;Title: Characterization of a highly toxic, large molecular size heat-stable enterotoxin
A;Reference number: S68705; MUID:95246844; PMID:7729521
A;Accession: S68705

```
A:Molecule type: protein
A:Residues: 1-53 <YOS>
A:Experimental source: strain 86-11
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:41-46,42-50,45-53/Disulfide bonds: #status predicted

Query Match      70.6%; Score 89; DB 2; Length 53;
Best Local Similarity 72.2%; Pred. No. 0.0012;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 NSSNYCCCLCCNPACNGC 18
    |:::|||||
Db 36 NDWDCCCLCCNPACFGC 53

RESULT 6
S31652
enterotoxin - Yersinia kristensenii
C:Species: Yersinia kristensenii
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S31652
R:Ibrahim, A.; Liesack, W.; Stackebrandt, E.
submitted to the EMBL Data Library, November 1992
A:Reference number: S31652
A:Accession: S31652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-66 <IBR>
A:Cross-references: UNIPROT:P31518; EMBL:X69218; NID:g48617; PIDN:CAA49152.1; PID:g48618
C:Superfamily: heat-stable enterotoxin ST

Query Match      69.8%; Score 88; DB 2; Length 66;
Best Local Similarity 75.0%; Pred. No. 0.0017;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 3 SNYCCCLCCNPACNGC 18
    |:::|||||
Db 51 SDWCCEVCNCPACAGC 66

RESULT 7
QHEC2
heat-stable enterotoxin ST-2 - Escherichia coli
C:Species: Escherichia coli
C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
C:Accession: A01823
R:Chan, S.K.; Giannella, R.A.
J. Biol. Chem. 256, 7744-7746, 1981
A:Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat
A:Reference number: A01823; MUID:81264141; PMID:7021541
A:Accession: A01823
A:Molecule type: protein
A:Residues: 1-18 <CHA>
A:Cross-references: UNIPROT:P01560
A:Experimental source: strain 18D, serotype 0.42:k86:H37
C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced by
ides of the heat-stable enterotoxin ST-I.
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
F:5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match      65.9%; Score 83; DB 1; Length 18;
Best Local Similarity 85.7%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 YCCCLCCNPACNGC 18
    ||||||
Db 4 YCCCLCCYPACAGC 17

RESULT 8
```

```
A54534
heat-stable enterotoxin - Vibrio mimicus (fragment)
C:Species: Vibrio mimicus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996
C:Accession: A54534
R:Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.
FEMS Microbiol. Lett. 79, 105-110, 1991
A:Title: Purification and characterization of a heat-stable enterotoxin of Vibrio mimicu
A:Reference number: A54534
A:Accession: A54534
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <ARI>
C:Superfamily: heat-stable enterotoxin ST

Query Match      64.3%; Score 81; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 0.0045;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 6 CCELCNCPACNGC 18
    |:::|||||
Db 3 CCEICNCPACFGC 15

RESULT 9
QHVC1
heat-stable enterotoxin ST precursor - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 17-Mar-1987 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41469; A01824; S34464; S34465; S34463
R:Ogawa, A.; Kato, J.I.; Watanabe, H.; Nair, B.G.; Takeda, T.
Infect. Immun. 58, 3325-3329, 1990
A:Title: Cloning and nucleotide sequence of a heat-stable enterotoxin gene from Vibrio c
A:Reference number: A41469; MUID:90382953; PMID:2205577
A:Accession: A41469
A:Molecule type: DNA
A:Residues: 1-78 <OGA>
A:Cross-references: UNIPROT:P04429; GB:M85198; GB:M36061; NID:g155237; PIDN:AAA64889.1;
R:Takao, T.; Shimonishi, Y.; Kobayashi, M.; Nishimura, O.; Arita, M.; Takeda, T.; Honda,
FEBS Lett. 193, 250-254, 1985
A:Title: Amino acid sequence of heat-stable enterotoxin produced by Vibrio cholerae non-
A:Reference number: A01824; MUID:86056320; PMID:4065341
A:Accession: A01824
A:Molecule type: protein
A:Residues: 62-78 <TAK>
A:Experimental source: non-O:1 serovar
R:Yoshino, K.; Miyachi, M.; Takao, T.; Bag, P.K.; Xiaozhe, H.; Nair, G.B.; Takeda, T.; S
FEBS Lett. 326, 83-86, 1993
A:Title: Purification and sequence determination of heat-stable enterotoxin elaborated b
A:Reference number: S34463; MUID:93314823; PMID:8325391
A:Accession: S34464
A:Status: preliminary
A:Molecule type: protein
A:Residues: 61-78 <YO3>
A:Accession: S34466
A:Status: preliminary
A:Molecule type: protein
A:Residues: 51-78 <YOS>
A:Accession: S34465
A:Status: preliminary
A:Molecule type: protein
A:Residues: 60-78 <YO2>
A:Accession: S34463
A:Status: preliminary
A:Molecule type: protein
A:Residues: 62-78 <YO4>
C:Superfamily: heat-stable enterotoxin ST
C:Keywords: enterotoxin; heat-stable protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:13-61/Domain: propeptide #status predicted <PRO>
F:62-78/Product: heat-stable enterotoxin ST #status experimental <MAT>
F:64-69,65-73,68-76/Disulfide bonds: #status predicted
```

Query Match 64.3%; Score 81; DB 1; Length 78;
 Best Local Similarity 84.6%; Pred. No. 0.01; 1; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCELCNPNACNGC 18
 |||:|||||||
 Db 64 CCEICCNPCGCG 76
 |||:|||||||

RESULT 10
 S25659
 heat-stable enterotoxin yst precursor - Yersinia enterocolitica
 C:Species: Yersinia enterocolitica
 C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: S25659; A41474; A23114; S65849
 R:Ibrahim, A.; Liesack, W.; Pike, S.; Stackebrandt, E.
 FEMS Microbiol. Lett. 97, 63-66, 1992
 A:Title: The polymerase chain reaction: an epidemiological tool to differentiate between
 A:Reference number: S25659
 A:Accession: S25659
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-71 <IBR>
 A:Cross-references: UNIPROT:P07593; EMBL:X65999; NID:G48611; PIDN:CAA46801.1; PID:G48612
 R:Delor, I.; Kaeckenbeeck, A.; Wauters, G.; Cornelis, G.R.
 Infect. Immun. 58, 2983-2988, 1990
 A:Title: Nucleotide sequence of yst, the Yersinia enterocolitica gene encoding the heat-
 A:Reference number: A41474; MUID:90354067; PMID:2201642
 A:Accession: A41474
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-47, 'S', 49-71
 A:Cross-references: GB:U09235; NID:G487394; PIDN:AAA18472.1; PID:G487395
 R:Takao, T.; Tomimaga, N.; Yoshimura, S.; Shimonishi, Y.; Hara, S.; Inoue, T.; Miyama, A.
 Eur. J. Biochem. 152, 199-206, 1985
 A:Title: Isolation, primary structure and synthesis of heat-stable enterotoxin produced
 A:Reference number: A23114; MUID:86004705; PMID:4043080
 A:Accession: A23114
 A:Molecule type: protein
 A:Residues: 54-71 <TAQ>
 R:Mikulakis, A.V.; Delor, I.; Ha Thi, V.; Cornelis, G.R.
 Mol. Microbiol. 14, 905-915, 1994
 A:Title: Regulation of the Yersinia enterocolitica enterotoxin yst gene. Influence of g
 A:Reference number: S65849; MUID:95231297; PMID:7715452
 A:Accession: S65849
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-43 <MIK>
 A:Cross-references: EMBL:U09235
 C:Genetics:
 A:Gene: yst
 C:Superfamily: heat-stable enterotoxin ST
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-41/Domain: propeptide #status predicted <PRO>
 F:42-71/Product: heat-stable enterotoxin yst #status predicted <MAT>

Query Match 62.3%; Score 78.5; DB 2; Length 71;
 Best Local Similarity 66.7%; Pred. No. 0.02; 4; Mismatches 1; Indels 1; Gaps 1;
 Matches 12; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 2 SSNY-CCELCNPNACNGC 18
 |||:|||||||
 Db 54 SSDWDCCDVCCNPACAGC 71
 |||:|||||||

RESULT 11
 S34671
 heat-stable enterotoxin - Vibrio cholerae (fragment)
 C:Species: Vibrio cholerae
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S34671
 R:Rossolini, G.M.; Lombardi, G.; Guglielmetti, P.
 submitted to the EMBL Data Library, July 1993

A;Description: Detection of the Vibrio cholerae heat-stable enterotoxin gene by polymera
 A;Reference number: S34671
 A;Accession: S34671
 A;Status: preliminary
 A:Molecule type: DNA
 A;Residues: 1-65 <ROS>
 A;Cross-references: UNIPROT:Q56643; EMBL:X74108
 C;Superfamily: heat-stable enterotoxin ST

Query Match 54.8%; Score 69; DB 2; Length 65;
 Best Local Similarity 90.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCELCNPNAC 15
 |||:|||||||
 Db 55 CCEICCNPCAC 64
 |||:|||||||

RESULT 12
 A45910
 ultra-high-sulfur keratin - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
 C:Accession: A45910
 R:McNab, A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.
 J. Invest. Dermatol. 92, 263-266, 1989
 A:Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.
 A:Reference number: A45910; MUID:89140394; PMID:2465353
 A:Accession: A45910
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-186 <MCN>
 A:Cross-references: UNIPROT:Q64526; GB:M27685; NID:G341749; PIDN:AAA81560.1; PID:G106681
 C:Superfamily: ultra-high-sulfur keratin

Query Match 49.6%; Score 62.5; DB 2; Length 186;
 Best Local Similarity 45.5%; Pred. No. 2.2; 3; Indels 7; Gaps 1;
 Matches 10; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

QY 5 YCELCNPNACNG-----CY 19
 : || ||| |||: ||
 Db 140 FCLNLCQPCAGSPVTCRTCY 161
 : || ||| |||: ||

RESULT 13
 JC4651
 uroguanylin precursor - human
 N:Alternate names: guanylyl cyclase activating peptide II
 C:Species: Homo sapiens (man)
 C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C:Accession: JC4651; S63702; S68052
 R:Miyaoto, M.; Nakazato, M.; Yamaguchi, H.; Date, Y.; Kojima, M.; Kangawa, K.; Matsuo, I.
 Biochem. Biophys. Res. Commun. 219, 644-648, 1996
 A:Title: Cloning and characterization of a cDNA encoding a precursor for human uroguanylin
 A:Reference number: JC4651; MUID:96193705; PMID:8605041
 A:Accession: JC4651
 A:Molecule type: mRNA
 A:Residues: 1-112 <MIY>
 A:Cross-references: UNIPROT:Q16661; GB:U34279; NID:G1236798; PIDN:AAAC50416.1; PID:G123679
 R:Hall, O.; Cetin, Y.; Cieslak, A.; Maegert, H.J.; Forssmann, W.G.
 Biochim. Biophys. Acta 1253, 146-149, 1995
 A:Title: A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): precurs
 A:Reference number: S63702; MUID:96106424; PMID:8519795
 A:Accession: S63702
 A:Molecule type: mRNA
 A:Residues: 1-112 <HIL>
 A:Cross-references: EMBL:Z50753; NID:G974823; PIDN:CAA90629.1; PID:G974824
 A:Experimental source: tissue colon
 R:Hess, R.; Kuhn, M.; Schulz-Knappe, P.; Raida, M.; Fuchs, M.; Klodt, J.; Adermann, K.; R
 FEBS Lett. 374, 34-38, 1995
 A:Title: GCAP-II: isolation and characterization of the circulating form of human uroguar
 A:Reference number: S68052; MUID:96049550; PMID:7589507
 A:Accession: S68052

A:Molecule type: protein
A:Residues: 89-99, 'X', 101-102, 'X', 104-107, 'X', 109-110, 'X', 112 <HES>
C:Comment: This protein, a member of the guanylin peptide family, is an endogenous activ
C:Superfamily: guanylin
C:Keywords: intestine
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-112/Product: uroguanylin #status predicted <MAT>

Query Match 46.8%; Score 59; DB 2; Length 112;
Best Local Similarity 62.5%; Pred. No. 3.8;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 SNYCCELCCNPACNGC 18
Db 96 ANDDCELCVNVACTGC 111

RESULT 14
JC7620
guanylin precursor, long form - European eel
C:Species: Anguilla anguilla (European eel)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
C:Accession: JC7620
R:Comrie, M.M.; Cutler, C.P.; Cramb, G.
Biochem. Biophys. Res. Commun. 281, 1078-1085, 2001
A:Title: Cloning and expression of guanylin from the European eel (Anguilla anguilla).
A:Reference number: JC7620; MUID:21139737; PMID:11243845
A:Accession: JC7620
A:Molecule type: mRNA
A:Residues: 1-116 <COM>
A:Cross-references: GB:AJ301673
C:Comment: This protein, a member of a family of heat-stable peptides, is a potent extra
axis. This peptide signalling system plays a role in osmoregulation in euryhaline teleo
C:Superfamily: guanylin
C:Keywords: heat-stable protein; osmoregulation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-116/Product: guanylin precursor, long form #status predicted <MAT>
F:33-39/Region: homologous #status predicted
F:69-114/Region: highly conserved #status predicted

Query Match 46.0%; Score 58; DB 2; Length 116;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CELCCNPACNGC 18
Db 104 CEICANAACTGC 115

RESULT 15
JC6548
high sulfur protein B2F - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: JC6548
R:Mitsui, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tauboi, R.; Ogawa, H.
Gene 208, 123-129, 1998
A:Title: Structure and hair follicle-specific expression of genes encoding the rat high
A:Reference number: JC6547; MUID:98201605; PMID:9524245
A:Accession: JC6548
A:Molecule type: DNA
A:Residues: 1-122 <MIT>
A:Cross-references: UNIPROT:O70149; DBJ:AB003753; NID:G3046870; PIDN:BAA25574.1; PID:G3
C:Comment: This protein is a cysteine-rich, keratin associated protein.
C:Genetics:
A:Gene: b2F
C:Superfamily: keratin high-sulfur matrix protein IIIA

Query Match 43.3%; Score 54.5; DB 2; Length 122;
Best Local Similarity 56.2%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 4 NYCCELCCNPACNGCY 19
Db 106 SYCGQSCCRPAC-CCY 120

Search completed: March 26, 2005, 16:49:39
Job time : 4.0219 secs

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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:18 ; Search time 16.365 Seconds
(without alignments)
594.533 Million cell updates/sec

Title: US-10-775-481A-5

Perfect score: 126

Sequence: 1 NSSNYCCCLCCNPACNGCY 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	95.2	61	QVEG8	Qveg8 escherichia
2	120	95.2	72	HST2_ECOLI	Q47185 escherichia
3	120	95.2	72	HST3_ECOLI	P07965 escherichia
4	116	92.1	61	QVEG7	Qveg7 escherichia
5	103	81.7	72	HST1_ECOLI	P01559 escherichia
6	98	77.8	18	Q7M0U3	Q7m0u3 citrobacter
7	95	75.4	61	QVEG9	Qveg9 escherichia
8	89	70.6	72	HSTC_YEREN	O50319 yersinia en
9	88	69.8	66	HST_YERKR	P31518 yersinia kr
10	85	67.5	71	HSTB_YEREN	P74977 yersinia en
11	83	65.9	18	HSTB_ECOLI	P01560 escherichia
12	81	64.3	17	Q8R581	Q8r581 vibrio chol
13	81	64.3	18	Q8R580	Q8r580 vibrio chol
14	81	64.3	19	Q8R579	Q8r579 vibrio chol
15	81	64.3	28	Q8R578	Q8r578 vibrio chol
16	81	64.3	78	HSTN_VIBCH	P04429 vibrio chol
17	81	64.3	78	HSTO_VIBCH	Q07425 vibrio chol
18	78.5	62.3	71	HSTA_YEREN	P07593 yersinia en
19	72	57.1	66	Q56643	Q56643 vibrio chol
20	72	57.1	78	Q93G01	Q93g01 vibrio mimi
21	62.5	49.6	186	Q64526	Q64526 mus musculu
22	62.5	49.6	191	Q9D3H7	Q9d3h7 mus musculu
23	62.5	49.6	195	Q9D141	Q9d141 mus musculu
24	61	48.4	118	Q8WT16	Q8wt16 dirosophila
25	61	48.4	197	Q86144	Q86144 dictyosteli
26	59	46.8	105	Q9BYP8	Q9byp8 homo sapien
27	59	46.8	112	GUAU_HUMAN	Q16661 homo sapien
28	58	46.0	106	GUAU_MOUSE	O90511 mus musculu
29	58	46.0	106	1	P70668 rattus norv
30	58	46.0	106	Q9QUQ3	Q9quq3 mus musculu
31	58	46.0	107	Q8R5G8	Q8r5g8 notomys ale

32	58	46.0	108	2	Q98TI0	Q98ti0 anguilla an
33	58	46.0	108	2	Q7ZZS0	Q7zzs0 anguilla ja
34	58	46.0	109	1	GUAU_DIDMA	Q28358 didelphis m
35	58	46.0	113	1	GUAU_PIG	O13009 sus scrofa
36	58	46.0	116	2	Q98TH9	Q98th9 anguilla an
37	58	46.0	167	2	Q9D122	Q9d122 mus musculu
38	57	45.2	111	1	GUAU_CAVPO	P70107 cavia porce
39	57	45.2	154	1	KR99_HUMAN	Q9byp9 homo sapien
40	56	44.4	168	2	Q9D732	Q9d732 mus musculu
41	56	44.4	426	2	Q67U09	Q67u09 oryza sativ
42	55.5	44.0	106	2	Q9QYU5	Q9qyu5 rattus norv
43	55	43.7	111	1	KR95_HUMAN	Q9byq1 homo sapien
44	55	43.7	154	1	KR94_HUMAN	Q9byq2 homo sapien
45	55	43.7	159	1	KR93_HUMAN	Q9byq3 homo sapien

ALIGNMENTS

RESULT 1

Q6VEG8	Q6VEG8	PRELIMINARY;	PRT;	61 AA.
AC	Q6VEG8;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Heat-stable enterotoxin ST Ib (Fragment).			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C4046;			
RX	PubMed=15364595;			
RA	Reischl U., Foussef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;			
RT	"Real-time fluorescence PCR assays for detection and characterization			
RT	of heat-labile I and heat-stable I enterotoxin genes from			
RT	enterotoxigenic Escherichia coli."			
RL	J. Clin. Microbiol. 42:4092-4100(2004).			
DR	EMBL; AY342058; AAQ92975.1;			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0009405; P:pathogenesis; IEA.			
DR	InterPro; IPR001489; Enterotoxin HS.			
DR	Pfam; PF02048; Enterotoxin HS; 1.			
DR	PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.			
FT	NON_TER			
SQ	SEQUENCE 61 AA; 6658 MW; 1D75955D7AF0DED2 CRC64;			

Query Match 95.2%; Score 120; DB 2; Length 61;
Best Local Similarity 94.7%; Pred. No. 9.7e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	NSSNYCCCLCCNPACNGCY	19
Db	43	NSSNYCCCLCCNPACTGCG	61

RESULT 2

ID	HST2_ECOLI	STANDARD;	PRT;	72 AA.
AC	Q47185;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Heat-stable enterotoxin A2 precursor (STA2).			
GN	Name=sta2;			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

```

RX MEDLINE=89108616; PubMed=2643580;
RA Guzman-Verdudio L.M., Kupersztoch Y.M.;
RT "Rectification of two Escherichia coli heat-stable enterotoxin allele
RT sequences and lack of biological effect of changing the carboxy-
RL terminal tyrosine to histidine.";
CC Infect. Immun. 57:645-648(1989).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC
CC EMBL: M18345; AAA23729.1; -.
CC PIR: J50292; QHECIB.
CC HSP: P01559; IETN.
CC InterPro: IPR001489; Enterotoxin HS.
CC Pfam: PF02048; Enterotoxin HS; 1.
CC PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
CC Enterotoxin; Signal; Toxin.
CC SIGNAL 1 19 Potential.
CC PROPEP 20 53 By similarity.
CC PPTIDE 54 72 Heat-stable enterotoxin A2.
CC DISULFID 59 64 By similarity.
CC DISULFID 60 68 By similarity.
CC DISULFID 63 71 By similarity.
CC SEQUENCE 72 AA; 7895 MW; D87850306E06260 CRC64;
Query Match 95.2%; Score 120; DB 1; Length 72;
Best Local Similarity 94.7%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NSSNYCCCLCCNPACNGCY 19
Db 54 NSSNYCCCLCCNPACTGCY 72
RESULT 3
HST3_ECOLI STANDARD; PRT; 72 AA.
AC P07965; P26588;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin A3/A4 precursor (STA3/STA4) (ST-IB) (ST-H).
GN Name=sta3; Synonyms=sta4;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89202548; PubMed=3071819;
RA Stieglitz H., Cervantes L., Robledo R., Fonseca R., Covarrubias L.,
RA Bolivar F., Kupersztoch Y.M.;
RT "Cloning, sequencing, and expression in ficoll-generated minicells of
RT an Escherichia coli heat-stable enterotoxin gene.";
RL Plasmid 20:42-53(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83184648; PubMed=6341230;
RA Moseley S.L., Hardy J.W., Huq M.I., Echeverria P., Falkow S.;
RT "Isolation and nucleotide sequence determination of a gene encoding a
RT heat-stable enterotoxin of Escherichia coli.";
RL Infect. Immun. 39:1167-1174(1983).

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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90273381; PubMed=2190361; DOI=10.1016/0041-0101(90)90085-L;
RA Zhou X., Shen L.P., Chi C.W.;
RT "Isolation and nucleotide sequence determination of a gene encoding a
RT heat-stable enterotoxin of Escherichia coli.";
RL Toxicon 28:453-456(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89108616; PubMed=2643580;
RA Guzman-Verdudio L.M., Kupersztoch Y.M.;
RT "Rectification of two Escherichia coli heat-stable enterotoxin allele
RT sequences and lack of biological effect of changing the carboxy-
RT terminal tyrosine to histidine.";
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=90034194; PubMed=2680769; DOI=10.1016/0378-1119(89)90182-0;
RA Dwarkanath P., Visweswariah S.S., Subrahmanyam Y.V.B.K., Shanthi G.,
RA Jagannatha H.M., Balganes T.S.;
RT "Cloning and hyperexpression of a gene encoding the heat-stable toxin
RT of Escherichia coli.";
RL Gene 81:219-226(1989).
RN [6]
RP SEQUENCE OF 54-72.
RX MEDLINE=83105138; PubMed=6759126;
RA Aimoto S., Takao T., Shimonishi Y., Hara S., Takeda T., Takeda Y.,
RA Miwatani T.;
RT "Amino-acid sequence of a heat-stable enterotoxin produced by human
RT enterotoxigenic Escherichia coli.";
RL Eur. J. Biochem. 129:257-263(1982).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
RA Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)
RT produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170(1987).
RN [8]
RP PROCESSING.
RX MEDLINE=90251166; PubMed=2187146;
RA Rasheed J.K., Guzman-Verdudio L.M., Kupersztoch Y.M.;
RT "Two precursors of the heat-stable enterotoxin of Escherichia coli:
RT evidence of extracellular processing.";
RL Mol. Microbiol. 4:265-273(1990).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC
CC EMBL: J03311; AAA24652.1; -.
CC EMBL: M34916; AAA23990.1; -.
CC EMBL: M18346; AAA23730.1; -.
CC EMBL: M29255; AAA24686.1; -.
CC PIR: J50292; QHECIB.
CC PIR: J70373; QHEC4.
CC HSP: P01559; IETN.
CC InterPro: IPR001489; Enterotoxin HS.
CC Pfam: PF02048; Enterotoxin HS; 1.
CC PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
CC Direct protein sequencing; Enterotoxin; Signal; Toxin.
CC SIGNAL 1 19
CC PROPEP 20 53

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FT PEPTIDE 54 72 Heat-stable enterotoxin A3/A4.
FT DISULFID 59 64
FT DISULFID 60 68
FT DISULFID 63 71
FT CONFLICT 19 19 A -> P (in Ref. 2).
SQ SEQUENCE 72 AA; 7909 MW; 1C5C9292BFCBA6BA CRC64;

Query Match 95.2%; Score 120; DB 1; Length 72;
Best Local Similarity 94.7%; Pred. NO. 1.1e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACTGCGY 19
Db 54 NSSNYCCCLCCNPACTGCGY 72

RESULT 4
Q6VEG7 PRELIMINARY; PRT; 61 AA.
ID Q6VEG7
AC Q6VEG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Heat-stable enterotoxin ST 1b (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R544;
RX PubMed=15364995;
RA Reischl U., Yousef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
RT of heat-labile I and heat-stable I enterotoxin genes from
RT enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).
DR EMBL; AY342059; AAQ92976.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
FT NON TER 1
FT TER 1
SQ SEQUENCE 61 AA; 6556 MW; 89788D3FAB3DCA0A CRC64;

Query Match 92.1%; Score 116; DB 2; Length 61;
Best Local Similarity 89.5%; Pred. NO. 3e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NSSNYCCCLCCNPACTGCGY 19
Db 43 NSSNYCCCLCCNPACTGCGY 61

RESULT 5
HST1_ECOLI STANDARD; PRT; 72 AA.
ID _HST1_ECOLI
AC P01559; Q47653;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Heat-stable enterotoxin ST-1A/ST-P precursor.
GN Name=st1;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Tn1681;
RX MEDLINE=81054703; PubMed=6254008;
RA So M., McCarthy B.J.;

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RT "Nucleotide sequence of the bacterial transposon Tn1681 encoding a
RT heat-stable (ST) toxin and its identification in enterotoxigenic
RT Escherichia coli strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4011-4015(1980).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O42:K86:H37 / 18D / ETEC;
RX MEDLINE=90368614; PubMed=2203756;
RA Dallas W.S.;
RT "The heat-stable toxin I gene from Escherichia coli 18D.";
RL J. Bacteriol. 172:5490-5493(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=85249571; PubMed=2990268;
RA Sekizaki T., Akashi H., Terakado N.;
RT "Nucleotide sequences of the genes for Escherichia coli heat-stable
RT enterotoxin I of bovine, avian, and porcine origins.";
RL Am. J. Vet. Res. 46:909-912(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Almoto S., Takeda T.,
RA Mawatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (StH)
RT produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170(1987).
RN [5]
RP PROCESSING.
RC MEDLINE=90368584; PubMed=2203746;
RA Okamoto K., Takahara M.;
RT "Synthesis of Escherichia coli heat-stable enterotoxin STp as a pre-
RT pro form and role of the pro sequence in secretion.";
RL J. Bacteriol. 172:5260-5265(1990).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (0.89 ANGSTROMS) OF 59-71.
RX MEDLINE=94312375; PubMed=8038153;
RA Sato T., Ozaki H., Hata Y., Kitagawa Y., Katsube Y., Shimonishi Y.;
RT "Structural characteristics for biological activity of heat-stable
RT enterotoxin produced by enterotoxigenic Escherichia coli: X-ray
RT crystallography of weakly toxic and nontoxic analogs.";
RL Biochemistry 33:8641-8650(1994).
CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC
CC EMBL; V00612; CAA23883.1; -.
CC EMBL; M58746; AAA62776.1; -.
CC EMBL; M25607; AAA24653.1; -.
CC PIR; A01822; QHEC1.
CC PDB; 1ETL; X-ray; @=59-71.
CC PDB; 1ETW; X-ray; @=..
CC PDB; 1ETN; X-ray; @=..
CC InterPro; IPR001489; Enterotoxin HS.
CC Pfam; PF02048; Enterotoxin HS; 1.
CC PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW 3D-structure; Enterotoxin; Signal; Toxin; Transposable element.
FT SIGNAL 1 19
FT PROPEP 20 54 Heat-stable enterotoxin ST-1A/ST-P.
FT PEPTIDE 55 72
FT DISULFID 59 64
FT DISULFID 60 68
FT DISULFID 63 71
FT CONFLICT 70 70 G -> P (in Ref. 3).

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FT TURN 61 62
FT TURN 66 67
FT TURN 69 70
SQ SEQUENCE 72 AA; 8075 MW; 9288B766B398264 CRC64;

Query Match 81.7%; Score 103; DB 1; Length 72;
Best Local Similarity 78.9%; Pred. No. 1.3e-05;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
  ::||| ||||| ||||| |||
Db 54 NNTFYCCCLCCNPACAGCY 72

RESULT 6
Q7M0U3 PRELIMINARY; PRT; 18 AA.
ID Q7M0U3
AC Q7M0U3
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Heat-stable enterotoxin ST-1a.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE
RX MEDLINE=89108617; PubMed=2912902;
RA Guarino A., Giannella R., Thompson M.R.;
RT "Citrobacter freundii produces an 18-amino-acid heat-stable
RT enterotoxin identical to the 18-amino-acid Escherichia coli heat-
RT stable enterotoxin (ST 1a).";
RL Infect. Immun. 57:649-652(1989).
DR PIR; A60103; A60103.
DR HSP; P01559; IETN.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;

Query Match 77.8%; Score 98; DB 2; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 YCCCLCCNPACNGCY 19
  ||||| ||||| |||||
Db 4 YCCCLCCNPACAGCY 18

RESULT 7
Q6VEG9 PRELIMINARY; PRT; 61 AA.
ID Q6VEG9
AC Q6VEG9;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Heat-stable enterotoxin ST-1a (fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=F7682;
RX PubMed=15364995;
RA Reischl U., Youssef M.T., Wolf H., Hyttia-Trees E., Strockbine N.A.;
RT "Real-time fluorescence PCR assays for detection and characterization
RT of heat-labile I and heat-stable I enterotoxin genes from
RT enterotoxigenic Escherichia coli.";
RL J. Clin. Microbiol. 42:4092-4100(2004).

DR EMBL; AY342057; AAQ92974.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin HS.
DR Pfam; PF02048; Enterotoxin HS; 1.
FT NON TER 1
SQ SEQUENCE 61 AA; 6927 MW; 646D4AE2F899D957 CRC64;

Query Match 75.4%; Score 95; DB 2; Length 61;
Best Local Similarity 73.7%; Pred. No. 0.00011;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NSSNYCCCLCCNPACNGCY 19
  ::||| ||||| ||||| |||
Db 43 NNTFYCCCLCCNPACAPCY 61

RESULT 8
HSTC YEREN
ID HSTC YEREN STANDARD; PRT; 72 AA.
AC Q50319;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat-stable enterotoxin C precursor (Y-STC).
GN Name=yetC;
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=86-11;
RX MEDLINE=97202479; PubMed=9049998; DOI=10.1006/mpat.1996.0094;
RA Huang X., Yoshino K., Nakao H., Takeda T.;
RT "Nucleotide sequence of a gene encoding the novel Yersinia
RT enterocolitica heat-stable enterotoxin that includes a pro-region-like
RT sequence in its mature toxin molecule.";
RL Microb. Pathog. 22:89-97(1997).
RN [2]
RP SEQUENCE OF 20-72.
RX STRAIN=Serotype O:3;
RX MEDLINE=95246844; PubMed=7729521; DOI=10.1016/0014-5793(95)00267-D;
RA Yoshino K., Takao T., Huang X., Murata H., Nakao H., Takeda T.,
RA Shimonishi Y.;
RT "Characterization of a highly toxic, large molecular size heat-stable
RT enterotoxin produced by a clinical isolate of Yersinia
RT enterocolitica.";
RL FEBS Lett. 362:319-322(1995).
CC -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC cyclase and increases cyclic GMP levels within the host intestinal
CC epithelial cells. Highly toxic.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
CC
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CC
CC EMBL; D63578; BAA23656.1; -.
CC HSP; P01559; IETN.
CC InterPro; IPR001489; Enterotoxin HS.
CC Pfam; PF02048; Enterotoxin HS; 1.
CC PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Direct protein sequencing; Enterotoxin; Signal; Toxin.
FT SIGNAL 1 19
FT CHAIN 20 72 Heat-stable enterotoxin C.
FT DISULFID 60 65 By similarity.
FT DISULFID 61 69 By similarity.

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FT  DISULFID 64 72  BY similarity.
SQ  SEQUENCE 72 AA; 7639 MW; 7C0D83893C2F981D CRC64;
Query Match 70.6%; Score 89; DB 1; Length 72;
Best Local Similarity 72.2%; Pred. No. 0.0007;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  1 NSSNYCCCLCCNPACNGC 18
DB  55 NDDWCCVCCNPACFGC 72

RESULT 9
HST_YERKR
ID  HST_YERKR STANDARD; PRT; 66 AA.
AC  P31518;
DT  01-JUL-1993 (Rel. 26, Created)
DT  01-JUL-1993 (Rel. 26, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Heat-stable enterotoxin precursor.
GN  Name=y8t;
OS  Yersinia kristensenii.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Yersinia.
OX  NCBI_TaxID=28152;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=IP490 / Serotype O:12,25;
RA  Ibrahim A., Liesack W., Stackebrandt G.;
RL  Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC  cyclase and increases cyclic GMP levels within the host intestinal
CC  epithelial cells (By similarity).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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EMBL; X69218; CRA49152.1; .
DR  PIR; S31652; S31652.
DR  HSSP; P01559; 1ETN.
DR  InterPro; IPR001489; Enterotoxin_HS.
DR  Pfam; PF02048; Enterotoxin_H; 1.
DR  PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW  Enterotoxin; Signal.
FT  SIGNAL 1 19 Potential.
FT  PROPEP 20 50
FT  CHAIN 51 66 Heat-stable enterotoxin (By similarity).
FT  DISULFID 54 59 By similarity.
FT  DISULFID 55 63 By similarity.
FT  DISULFID 58 66 By similarity.
SQ  SEQUENCE 66 AA; 7068 MW; 27BE7006675CC075 CRC64;

Query Match 69.8%; Score 88; DB 1; Length 66;
Best Local Similarity 75.0%; Pred. No. 0.00087;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY  3 SNYCCCLCCNPACNGC 18
DB  51 SDWCCVCCNPACAGC 66

RESULT 10
HSTB_YEREN
ID  HSTB_YEREN STANDARD; PRT; 71 AA.
AC  P74977;
DT  15-DEC-1998 (Rel. 37, Created)

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DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Heat-stable enterotoxin B precursor (Y-STB).
GN  Name=y8tB;
OS  Yersinia enterocolitica.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Yersinia.
OX  NCBI_TaxID=630;
RN  [1]
RP  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC  STRAIN=84-50 / Serotype O:5;
RX  MEDLINE=98008784; PubMed=9344780; DOI=10.1006/mpat.1997.0146;
RA  Ramamurthy T., Yoshino K., Huang X., Nair G.B., Carniel E.,
RA  Maruyama T., Fukushima H., Takeda T.;
RT  "The novel heat-stable enterotoxin subtype gene (y8tB) of Yersinia
RT  enterocolitica: nucleotide sequence and distribution of the yst
RT  genes";
RL  Microb. Pathog. 23:189-200(1997).
CC  -!- FUNCTION: Toxin which activates the particulate form of guanylate
CC  cyclase and increases cyclic GMP levels within the host intestinal
CC  epithelial cells. Could play an important role in pathogenesis.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.
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-----
EMBL; D88145; BAA13544.1; .
DR  HSSP; P01559; 1ETN.
DR  InterPro; IPR001489; Enterotoxin_HS.
DR  Pfam; PF02048; Enterotoxin_H; 1.
DR  PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW  Direct protein sequencing; Enterotoxin; Signal; Toxin.
FT  SIGNAL 1 19 Potential.
FT  PROPEP 20 52
FT  CHAIN 53 71 Heat-stable enterotoxin B.
FT  DISULFID 59 64 By similarity.
FT  DISULFID 60 68 By similarity.
FT  DISULFID 63 71 By similarity.
SQ  SEQUENCE 71 AA; 7670 MW; ED6B9F61ACDD4F50 CRC64;

Query Match 67.5%; Score 85; DB 1; Length 71;
Best Local Similarity 64.7%; Pred. No. 0.0021;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  2 SSNYCCCLCCNPACNGC 18
DB  55 NDDWCCVCCNPACAGC 71

RESULT 11
HSTB_ECOLI
ID  HSTB_ECOLI STANDARD; PRT; 18 AA.
AC  P01560;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Heat-stable enterotoxin ST-2 (ST-B).
OS  Escherichia coli.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=O42:K86:H37 / 18D / ETEC;
RX  MEDLINE=81264141; PubMed=7021541;
RA  Chan S.-K., Giannella R.A.;
RT  "Amino acid sequence of heat-stable enterotoxin produced by

```

RT Escherichia coli pathogenic for man.;"

RL J. Biol. Chem. 256:7744-7746(1981).

RN [2]

RP DISULFIDE BONDS.

RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;

RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,

RA Miwatani T., Takeda Y.;

RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)

RT produced by a human strain of enterotoxigenic Escherichia coli.;"

RL FEBS Lett. 215:165-170(1987).

CC -!- FUNCTION: Toxin which activates the particulate form of guanylate

CC cyclase and increases cyclic GMP levels within the host intestinal

CC epithelial cells.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.

DR FIR; A01823; QHEC2.

DR HSSP; P01559; 1ETN.

DR InterPro; IPR001489; Enterotoxin_HS.

DR Pfam; PF02048; Enterotoxin_HS; 1.

DR PROSITE; PS00273; ENTEROTOXIN_H STABLE; 1.

KW Direct protein sequencing; Enterotoxin; Toxin.

FT DISULFID 5 10

FT DISULFID 6 14

FT DISULFID 9 17

SQ SEQUENCE 18 AA; 1978 MW; D0C975F49D600650 CRC64;

Query Match 65.9%; Score 83; DB 1; Length 18;

Best Local Similarity 85.7%; Pred. No. 0.0012; 2; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 2;

QY 5 YCCELCCNPACNGC 18
||||| ||| |||

DB 4 YCCELCCYPACAGC 17
||||| ||| |||

RESULT 12

Q9R581 Q9R581 PRELIMINARY; PRT; 17 AA.

AC Q9R581;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE 01-ST-1, NAG-ST, VN-ST=HEAT-stable enterotoxin.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE.

RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;

RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,

RA Takeda T., Shimonishi Y.;

RT "Purification and sequence determination of heat-stable enterotoxin

RT elaborated by a cholera toxin-producing strain of Vibrio cholerae

RT O1.;"

RL FEBS Lett. 326:83-86(1993).

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR001489; Enterotoxin_HS.

DR Pfam; PF02048; Enterotoxin_HS; 1.

DR PROSITE; PS00273; ENTEROTOXIN_H STABLE; 1.

SQ SEQUENCE 17 AA; 1821 MW; 30FF036D018D601C CRC64;

Query Match 64.3%; Score 81; DB 2; Length 17;

Best Local Similarity 84.6%; Pred. No. 0.002; 1; Indels 0; Gaps 0;

Matches 11; Conservative 1; Mismatches 1;

QY 6 CCELCNCPACNGC 18
||||| ||| |||

DB 3 CCEICCNPAFCG 15
||||| ||| |||

RESULT 13

Q9R580 Q9R580 PRELIMINARY; PRT; 18 AA.

AC Q9R580;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE 01-ST-2, VC-H-ST=HEAT-stable enterotoxin.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE.

RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;

RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,

RA Takeda T., Shimonishi Y.;

RT "Purification and sequence determination of heat-stable enterotoxin

RT elaborated by a cholera toxin-producing strain of Vibrio cholerae

RT O1.;"

RL FEBS Lett. 326:83-86(1993).

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR001489; Enterotoxin_HS.

DR Pfam; PF02048; Enterotoxin_HS; 1.

DR PROSITE; PS00273; ENTEROTOXIN_H STABLE; 1.

SQ SEQUENCE 18 AA; 1934 MW; 3080692D018D601C CRC64;

Query Match 64.3%; Score 81; DB 2; Length 18;

Best Local Similarity 84.6%; Pred. No. 0.0021; 1; Indels 0; Gaps 0;

Matches 11; Conservative 1; Mismatches 1;

QY 6 CCELCNCPACNGC 18
||||| ||| |||

DB 4 CCEICCNPAFCG 16
||||| ||| |||

RESULT 14

Q9R579 Q9R579 PRELIMINARY; PRT; 19 AA.

AC Q9R579;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE 01-ST-3=HEAT-stable enterotoxin.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE.

RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;

RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,

RA Takeda T., Shimonishi Y.;

RT "Purification and sequence determination of heat-stable enterotoxin

RT elaborated by a cholera toxin-producing strain of Vibrio cholerae

RT O1.;"

RL FEBS Lett. 326:83-86(1993).

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR001489; Enterotoxin_HS.

DR Pfam; PF02048; Enterotoxin_HS; 1.

DR PROSITE; PS00273; ENTEROTOXIN_H STABLE; 1.

SQ SEQUENCE 19 AA; 2048 MW; 308015F1A18D601C CRC64;

Query Match 64.3%; Score 81; DB 2; Length 19;

Best Local Similarity 84.6%; Pred. No. 0.0022; 1; Indels 0; Gaps 0;

Matches 11; Conservative 1; Mismatches 1;

QY 6 CCELCNCPACNGC 18
||||| ||| |||

DB 5 CCEICCNPAFCG 17
||||| ||| |||

```
RESULT 15
Q9RS78      Q9RS78      PRELIMINARY;      PRT;      28 AA.
AC Q9RS78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB 01-ST-4=HEAT-stable enterotoxin.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE.
RX MEDLINE=93314823; PubMed=8325391; DOI=10.1016/0014-5793(93)81766-S;
RA Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
RA Takeda T., Shimonishi Y.;
RT "Purification and sequence determination of heat-stable enterotoxin
RT elaborated by a cholera toxin-producing strain of Vibrio cholerae
RT O1.";
RL FEBS Lett. 326:83-86(1993).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SQ SEQUENCE 28 AA; 3080 MW; 25ECADAFBC57DB72 CRC64;

Query Match      64.3%; Score 81; DB 2; Length 28;
Best Local Similarity 84.6%; Pred. No. 0.0031;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CCELCNCPACNGC 18
Db     14 CCEICCNPACEGC 26
      |||:|||||
      |||:|||||

Search completed: March 26, 2005, 16:48:34
Job time : 16.365 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2005, 16:35:58 ; Search time 116.058 Seconds
(without alignments)
353.241 Million cell updates/sec

Title: US-10-775-481A-55
Perfect score: 548
Sequence: 1 MSGSQLAAVLLLVLSAQ.....LRTIATDECELCINACTGC 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	100.0	106	8	ADR45874 Amino aci
2	356	65.0	108	2	AAW18467 Human GCA
3	356	65.0	108	2	AAW18478 Human GCA
4	356	65.0	108	2	AAW23221 GCAP-II C
5	356	65.0	112	2	AAW18498 Human GCA
6	356	65.0	112	2	AAW10595 Guanylate
7	356	65.0	112	6	ABG74823 Human uro
8	356	65.0	112	8	ADR45875 Amino aci
9	304	55.5	84	2	AAW18484 Human GCA
10	304	55.5	84	2	AAW23232 GCAP-II C
11	292	53.3	81	2	AAW18485 Human GCA
12	292	53.3	81	2	AAW23233 GCAP-II C
13	280	51.1	78	2	AAW18486 Human GCA
14	280	51.1	78	2	AAW23234 GCAP-II C
15	279	50.9	77	2	AAW18468 Human GCA
16	279	50.9	77	2	AAW18479 Human GCA
17	279	50.9	77	2	AAW23222 GCAP-II C
18	261	47.6	73	2	AAW18490 Human GCA
19	261	47.6	73	2	AAW23237 GCAP-II C
20	252.5	46.1	109	6	ABG74824 Opossum l
21	251	45.8	70	2	AAW18471 Human GCA
22	251	45.8	70	2	AAW18480 Human GCA
23	251	45.8	70	2	AAW23225 GCAP-II C
24	246	44.9	69	2	AAW18472 Human GCA
25	246	44.9	69	2	AAW18481 Human GCA

26	246	44.9	69	2	AAW23226	GCAP-II C
27	241	44.0	67	2	AAW18474	Human GCA
28	241	44.0	67	2	AAW23228	GCAP-II C
29	239	43.6	66	2	AAW18491	Human GCA
30	239	43.6	66	2	AAW23238	GCAP-II C
31	236	43.1	69	2	AAW18488	Human GCA
32	234	42.7	64	2	AAW18492	Human GCA
33	234	42.7	64	2	AAW23239	GCAP-II C
34	228	41.6	56	2	AAW18469	Human GCA
35	228	41.6	56	2	AAW23223	GCAP-II C
36	195	35.6	43	2	AAW18489	Human GCA
37	195	35.6	43	2	AAW23236	GCAP-II C
38	175	31.9	38	2	AAW18475	Human GCA
39	175	31.9	38	2	AAW23229	GCAP-II C
40	169	30.8	37	2	AAW18493	Human GCA
41	169	30.8	37	2	AAW23240	GCAP-II C
42	166.5	30.4	115	2	AAW42460	Human gua
43	166.5	30.4	115	6	ABG74822	Rat and h
44	166.5	30.4	115	6	ABR58198	Human NOV
45	166.5	30.4	115	6	ADA10943	Human CDN

ALIGNMENTS

RESULT 1

ADR45874
ID ADR45874 standard; peptide; 106 AA.

AC ADR45874;

XX 18-NOV-2004 (first entry)

DE Amino acid sequence of ST receptor ligand uroguanylin.

XX heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
KW uroguanylin.

OS Rattus sp.

XX WO2004071436-A2.

XX 26-AUG-2004.

XX 10-FEB-2004; 2004WO-US003765.

XX 10-FEB-2003; 2003US-0446730P.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;

XX WPI; 2004-615913/59.

Increasing ST receptor molecules on the surface of a colorectal, gastric or esophageal cancer cell to treat these cancers comprises administering ST receptor ligand molecules that bind to ST receptors on the surface of the cancer cell.

Claim 6; SEQ ID NO 55; 97pp; English.

The specification describes a method for increasing the number of heat stable toxin (ST) receptor molecules on the surface of a metastasised colorectal cancer cell. The method comprises administering, by continuous infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight per hour for at least 6 hours, where ST receptor ligand molecules bind to ST receptors on the surface of the cancer cell in the individual and the number of ST receptor molecules on the surface of the cancer cell is increased. Therapeutic compositions comprising components which target ST receptors can then be used to inhibit proliferation of the colorectal, gastric and oesophageal cells. This method may be used for treating individuals that have diseases that affect colorectal, gastric and

CC oesophageal cells, including colorectal, gastric or oesophageal cancers.
CC The present sequence represents a ST receptor ligand used in the method
CC of the invention, designated uroguanylin.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 548; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.9e-54; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 0;

QY 1 MSGSQLAAVLLLLVLSAQGVYIKYHGFQVLESVKLNLEEEKQMSDPQOKSGLLPD 60
DB 1 MSGSQLAAVLLLLVLSAQGVYIKYHGFQVLESVKLNLEEEKQMSDPQOKSGLLPD 60
QY 61 VCNPALPLDLPVCASQEAASFTFKALRTIATDELCINVACTGC 106
DB 61 VCNPALPLDLPVCASQEAASFTFKALRTIATDELCINVACTGC 106

RESULT 2

AAW18467
ID AAW18467 standard; peptide; 108 AA.

AC AAW18467;

DT 23-APR-1998 (first entry)

DE Human GCAP-II (89-112) endoprotease Arg-C digested fragment 1.

KW Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
KW diabetes; endocrine disorder; diagnosis; treatment; human.

OS Homo sapiens.

PN DE19543628-A1.

XX 28-MAY-1997.

XX 24-NOV-1995; 95DE-01043628.

XX 24-NOV-1995; 95DE-01043628.

XX (FORS/) FORSMANN W.

PI Forsmann W, Kist A, Kruhoeffler M, Meyer M, Pardigol A, Heine G;

XX WPI; 1997-290350/27.

PT New guanyl cyclase C activating peptide fragments - have insulinotropic
PT activity, useful for treating diabetes, etc.

PS Claim 3; Fig 3; 33pp; German.

XX Peptides AAW18467-W18470 represent fragments of the guanyl cyclase C
CC activating peptide, GCAP-II, obtained by digestion with endoprotease Arg-
CC C. GCAP-II is involved in insulin secretion by pancreatic beta cells.
CC This peptide fragment could be used to which affects insulin secretion by
CC the beta cells treat pancreatic endocrine disorders, especially diabetes
CC mellitus type II, renal and intestinal disorders, disorders of the
CC gastrointestinal, respiratory and urogenital apparatus, disorders of the
CC cardiovascular and nervous systems, disorders of the integuments and
CC sense organs and diseases associated with GCAP II (89-112) deficiency.
CC This peptide can be used for treatment of electrolyte effects on bone
CC reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
CC -II (89-112) can be used to treat diseases associated with overproduction
CC of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
CC useful for diagnosis and treatment of the above disorders e.g. gene
CC therapy for diabetes

XX Sequence 108 AA;

Query Match 65.0%; Score 356; DB 2; Length 108;
Best Local Similarity 65.7%; Pred. No. 1.7e-32;

Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
QY 2 SGSQLAAVLLLLVLSAQGVYIKYHGFQVLESVKLNLEEEKQMSDPQOKSGLLPD 61
DB 3 SGLPGVAVVLLLLVLSAQGVYIKYHGFQVLESVKLNLEEEKQMSDPQOKSGLLPD 62
QY 62 CYNPALPLDLPVCASQEAASFTFKALRTIATDELCINVACTGC 106
DB 63 CHHPALPDLPVCASQEAASFTFKALRTIATDELCINVACTGC 107

RESULT 3

AAW18478

ID AAW18478 standard; peptide; 108 AA.

XX AAW18478;

XX 22-APR-1998 (first entry)

DE Human GCAP-II (89-112) trypsin digested fragment 1.

DE Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
KW diabetes; endocrine disorder; diagnosis; treatment; human.

OS Homo sapiens.

PN DE19543628-A1.

XX 28-MAY-1997.

XX 24-NOV-1995; 95DE-01043628.

XX 24-NOV-1995; 95DE-01043628.

XX (FORS/) FORSMANN W.

PI Forsmann W, Kist A, Kruhoeffler M, Meyer M, Pardigol A, Heine G;

XX WPI; 1997-290350/27.

PT New guanyl cyclase C activating peptide fragments - have insulinotropic
PT activity, useful for treating diabetes, etc.

PS Claim 3; Fig 3; 33pp; German.

XX Peptides AAW18478-W18483 represent fragments of the guanyl cyclase C
CC activating peptide, GCAP-II, obtained by digestion with trypsin. GCAP-II
CC is involved in insulin secretion by pancreatic beta cells. This peptide
CC fragment could be used to which affects insulin secretion by the beta
CC cells treat pancreatic endocrine disorders, especially diabetes mellitus
CC type II, renal and intestinal disorders, disorders of the respiratory,
CC gastrointestinal and urogenital apparatus, disorders of the
CC cardiovascular and nervous systems, disorders of the integuments and
CC sense organs and diseases associated with GCAP II (89-112) deficiency.
CC This peptide can be used for treatment of electrolyte effects on bone
CC reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
CC -II (89-112) can be used to treat diseases associated with overproduction
CC of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
CC useful for diagnosis and treatment of the above disorders e.g. gene
CC therapy for diabetes

XX Sequence 108 AA;

Query Match 65.0%; Score 356; DB 2; Length 108;
Best Local Similarity 65.7%; Pred. No. 1.7e-32;

Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
QY 2 SGSQLAAVLLLLVLSAQGVYIKYHGFQVLESVKLNLEEEKQMSDPQOKSGLLPD 61
DB 3 SGLPGVAVVLLLLVLSAQGVYIKYHGFQVLESVKLNLEEEKQMSDPQOKSGLLPD 62
QY 62 CYNPALPLDLPVCASQEAASFTFKALRTIATDELCINVACTGC 106

Qy	2	SGSOLAAVALLLVLSQAQGVYIKYHGFQVQLSVKKNLEEEKQMSDPQOQKSGLLPDV	61
Db	3	SGLLPGVAVVLLLLLSQTSQSVYIQGFRVQLSMKKLSDLAQWAPSPRLQAQSLIPAV	62
Qy	62	CYNPALPLDLPVCASQEAASSTFKALRTIATDECELCINVACTGC	106
Db	63	CHHPALPDLPVCASQEAASSIFKILRTIANDDCELCVNVACTGC	107
RESULT 5			
ID	AAW18498		
XX	AAW18498	standard; protein; 112 AA.	
XX	AAW18498;		
XX	22-APR-1998	(first entry)	
XX	Human GCAP-II	precursor protein.	
DE	XX		
XX	XX		
KW	XX	Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;	
KW	XX	diabetes; endocrine disorder; diagnosis; treatment; human.	
OS	XX	Homo sapiens.	
OS	XX		
PN	XX	DF19543628-A1.	
XX	XX		
PD	XX	28-MAY-1997.	
XX	XX		
PF	XX	24-NOV-1995; 95DE-01043628.	
XX	XX		
PR	XX	24-NOV-1995; 95DE-01043628.	
XX	XX		
PA	XX	(FORS/) FORSMANN W.	
XX	XX		
PI	XX	Forssmann W, Kist A, Kruhoeffer M, Meyer M, Pardigol A, Heine G;	
XX	XX		
WPI	XX	1997-290350/27.	
DR	XX	N-PSDB; AAT65115.	
DR	XX		
PT	XX	New guanyl cyclase C activating peptide fragments - have insulinotropic	
PT	XX	activity, useful for treating diabetes, etc.	
XX	XX		
PS	XX	Example 6; Fig 11; 33pp; German.	
XX	XX		
CC	XX	This sequence represents a precursor of the guanyl cyclase C activating	
CC	XX	peptide, GCAP-II, which affects insulin secretion by the beta cells in	
CC	XX	the pancreas. This peptide is useful for treating pancreatic endocrine	
CC	XX	disorders, especially diabetes mellitus type II, renal and intestinal	
CC	XX	disorders, disorders of the gastrointestinal, respiratory and urogenital	
CC	XX	apparatus, disorders of the cardiovascular and nervous systems, disorders	
CC	XX	of the integuments and sense organs and diseases associated with GCAP-II	
CC	XX	(89-112) deficiency. This peptide can be used for treatment of	
CC	XX	electrolyte effects on bone reconstruction (osteoporosis) or the dental	
CC	XX	apparatus. Antibodies to GCAP-II (89-112) can be used to treat diseases	
CC	XX	associated with overproduction of GCAP-II (89-112). Human GCAP-II (89-	
CC	XX	112) and GCAP-I (99-15) cDNA are useful for diagnosis and treatment of	
CC	XX	the above disorders e.g. gene therapy for diabetes	
XX	XX		
SQ	XX	Sequence 112 AA;	
Query Match 65.0%; Score 356; DB 2; Length 112;			
Best Local Similarity 65.7%; Pred. No. 1.8e-32;			
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0			
Qy	2	SGSOLAAVALLLVLSQAQGVYIKYHGFQVQLSVKKNLEEEKQMSDPQOQKSGLLPDV	61
Db	7	SGLLPGVAVVLLLLLSQTSQSVYIQGFRVQLSMKKLSDLAQWAPSPRLQAQSLIPAV	66
Qy	62	CYNPALPLDLPVCASQEAASSTFKALRTIATDECELCINVACTGC	106
Db	67	CHHPALPDLPVCASQEAASSIFKILRTIANDDCELCVNVACTGC	111

RESULT 6
AAW10595
ID AAW10595 standard; protein; 112 AA.
AC AAW10595;
XX
XX 29-OCT-1997 (first entry)
XX Guanylate cyclase activating peptide II.
XX
XX Human; guanylate cyclase; activating peptide; GCAP-II; cGMP;
KW trans epithelial transport; treatment; kidney; intestinal; respiratory;
KW urogenital; circulatory; nervous system; disorder; disease; endocrine;
KW sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis;
KW gastrointestinal tract; diarrhoea; gene therapy; probe;
KW recombinant production; transgenic animal; antibody; immunoassay reagent.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Peptide 1. .88
XX FT /label= sig_peptide
XX FT 89. .112
XX FT /label= mat_peptide
XX
XX DE19528544-A1.
XX
XX 06-FEB-1997.
XX
XX 03-AUG-1995; 95DE-01028544.
XX
XX 03-AUG-1995; 95DE-01028544.
XX (FORS/) FORSMANN W.
XX
XX Forsmann W;
XX
XX WPI; 1997-110032/11.
XX N-PSDB; AAT60819.
XX
XX Guanylate cyclase activating peptide II - increases cGMP formation, and
XX controls transport of water and electrolytes across epithelial cells.
XX
XX Claim 1; Page 4; 15pp; German.
XX
XX The present sequence is the human guanylate cyclase activating peptide II
XX (GCAP-II), which increases cGMP formation, and is involved in the control
XX of trans epithelial water and electrolyte transport. GCAP-II can be used
XX to treat a variety of kidney, intestinal, respiratory, urogenital,
XX circulatory and nervous system disorders, diseases of the endocrine and
XX sensory systems (e.g. osteoporosis, and dental disease), disorders of the
XX pancreas (e.g. diabetes, and hypophysis) or the endocrine
XX gastrointestinal tract and for the long term treatment of diarrhoea,
XX without inducing an immune response. The GCAP-II cDNA can be used to
XX treat the same conditions, clone the GCAP-II-encoding gene for use in
XX gene therapy, as a hybridisation probe and for the production of
XX recombinant GCAP-II or transgenic animal creation. Antibodies raised
XX against GCAP-II are useful as immunoassay reagents. GCAP-II is
XX administered at, e.g. 100-1200 microg/day by intravenous or intramuscular
XX injection or 300-1200 microg/day subcutaneously. It may also be given
XX orally, intranasally or by inhalation, in typical unit doses of 0.3-30
XX mg. GCAP-II was chemically synthesised, or isolated by chromatography
XX from transformed eukaryotic or prokaryotic cells, or human blood. When
XX T84 cells were incubated with synthetic GCAP-II, generation of cGMP was
XX increased in a dose dependent manner. GCAP-II influences cGMP production
XX via a known receptor for heat stable enterotoxin. Other stomach,
XX intestinal, pancreatic and liver cells also responded to GCAP-II, e.g.
XX via changes in intracellular Ca2+ ion concentration
XX
XX Sequence 112 AA;
XX
XX Query Match 65.0%; Score 356; DB 2; Length 112;
XX Best Local Similarity 65.7%; Pred. No. 1.8e-32;

Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
QY 2 SSSQLWAAVLLLVLSAQGVYIKYGFQVLESVKLEBEKQMSDFOQKSGLLPDV 61
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
7 SGLPGVAVVLLLLLSQTSQSVYIQGFRVLESMMKLSDEAQAAPSPRLQAQSLPAV 66
QY 62 CYNPALPLDLQPVCAQSEAASTFKALRTIATDELCINVACTGC 106
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
67 CHHPALPQDLQPVCAQSEASSIFKTURTIANDDCELCVNVACTGC 111
RESULT 7
ABG74823
ID ABG74823 standard; protein; 112 AA.
XX
XX AC ABG74823;
XX
XX DT 12-JUN-2003 (first entry)
XX Human uroguanylin precursor SEQ ID 5.
XX
XX DE Apical membrane; mucosal epithelial cell; respiratory tract;
XX KW guanylate cyclase C; G protein-coupled receptor; guanosine triphosphate;
KW cyclic guanosine monophosphate; cGMP; chloride ion secretion; inhalation;
KW membrane-associated type II protein kinase; mucus fluidisation;
KW cystic fibrosis transmembrane conductance regulator; breathing disorder;
KW mucus secretion; antiasthmatic; antiinflammatory; bronchial asthma;
KW chronic bronchitis; cystic fibrosis; uroguanylin; human.
XX
XX OS Homo sapiens.
XX
XX PN WO200298912-A2.
XX
XX PD 12-DEC-2002.
XX
XX 05-JUN-2002; 2002WO-DE002040.
XX
XX 05-JUN-2001; 2001DE-01027119.
XX (CENT/) CETIN Y.
XX (SAVA/) SAVAS Y.
XX
XX Cetin Y, Savas Y;
XX
XX WPI; 2003-156842/15.
XX
XX Composition useful for treating respiratory disease, comprises a peptide
XX that activates guanylate cyclase C, and is delivered to the apical
XX membrane through the respiratory tract.
XX
XX Claim 3; Page 3; 23pp; German.
XX
XX This invention describes a novel medicament in a formulation that is
XX delivered to the apical membrane of mucosal epithelial cells through the
XX respiratory tract. The medicament contains at least one peptide that
XX activates guanylate cyclase C (GCC). GCC is a G protein-coupled receptor
XX that catalyses conversion of guanosine triphosphate to cyclic guanosine
XX monophosphate (cGMP) and is present on the apical (air) side of
XX respiratory epithelial cells but not on the basolateral (blood) side.
XX cGMP activates membrane-associated type II protein kinase which in turn
XX activates the regulatory domain of the cystic fibrosis transmembrane
XX conductance regulator, resulting in secretion of chloride ions and water
XX from the cells, causing fluidisation of the mucus. The products of the
XX invention are used to make an inhalation device containing the medicament
XX for diagnosing diseases that are accompanied by breathing disorders or
XX disorders of mucus secretion in the respiratory tract, by detecting at
XX least one GCC activator. The products of the invention have antiasthmatic
XX and antiinflammatory activity. The method is useful for diagnosing and
XX treating diseases accompanied by breathing disorders or disorders of
XX mucus secretion in the respiratory tract particularly bronchial asthma,
XX chronic bronchitis and cystic fibrosis. The product of the invention
XX improves fluidity and evacuation of bronchial mucus and acts locally
XX (since the medicament does not enter the bloodstream), so systemic side

CC effects are minimised. Only very small doses of the medicament are required. This sequence represents a precursor of the human guanylate cyclase C activating peptide, uroguanylin, described in the disclosure of the invention

XX SQ Sequence 112 AA;

Query Match 65.0%; Score 356; DB 6; Length 112;
Best Local Similarity 65.7%; Pred. No. 1.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy 2 SGSQWAAVLLLVLSAQGVYIKYHGFQVLESVKKLNELEEKQMSDPQOKSGLLPDV 61
Db 7 SGLPGVAVVLLLLQSTQSVYIQGFRVLESMMKLSLEAQWAPSPRLQAOSSLPAV 66
Qy 62 CYNPALPLDLQPVCAQEAASFTFKALRTIATDECELCINVACTGC 106
Db 67 CHHPALPDQLQPVCAQEAASFTFKALRTIATDECELCINVACTGC 111

RESULT 8

ADR45875
ID ADR45875 standard; peptide; 112 AA.

XX ADR45875;

XX 18-NOV-2004 (first entry)

XX Amino acid sequence of ST receptor ligand uroguanylin.

XX heat stable toxin; ST; ST receptor; colorectal cancer; gastric cancer;
KW oesophageal cancer; colorectal cell; gastric cell; oesophageal cell;
KW uroguanylin.

XX Homo sapiens.

XX WO2004071436-A2.

XX 26-AUG-2004.

XX 10-FEB-2004; 2004WO-US003765.

XX 10-FEB-2003; 2003US-0446730P.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Waldman SA, Pitari GM, Park J, Schulz S, Wolfe HR;

XX WPI; 2004-615913/59.

XX Increasing ST receptor molecules on the surface of a colorectal, gastric
or esophageal cancer cell to treat these cancers comprises administering
ST receptor ligand molecules that bind to ST receptors on the surface of
the cancer cell.

XX Claim 6; SEQ ID NO 56; 97pp; English.

XX The specification describes a method for increasing the number of heat
stable toxin (ST) receptor molecules on the surface of a metastasised
colorectal cancer cell. The method comprises administering, by continuous
infusion, at least 0.1 nM of an ST receptor ligand per 10 kg bodyweight
per hour for at least 6 hours, where ST receptor ligand molecules bind to
ST receptors on the surface of the cancer cell in the individual and the
number of ST receptor molecules on the surface of the cancer cell is
increased. Therapeutic compositions comprising components which target ST
receptors can then be used to inhibit proliferation of the colorectal,
gastric and oesophageal cells. This method may be used for treating
individuals that have diseases that affect colorectal, gastric and
oesophageal cells, including colorectal, gastric or oesophageal cancers.
The present sequence represents a ST receptor ligand used in the method
of the invention, designated uroguanylin.

XX SQ Sequence 112 AA;

Query Match 65.0%; Score 356; DB 8; Length 112;
Best Local Similarity 65.7%; Pred. No. 1.8e-32;
Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy 2 SGSQWAAVLLLVLSAQGVYIKYHGFQVLESVKKLNELEEKQMSDPQOKSGLLPDV 61
Db 7 SGLPGVAVVLLLLQSTQSVYIQGFRVLESMMKLSLEAQWAPSPRLQAOSSLPAV 66
Qy 62 CYNPALPLDLQPVCAQEAASFTFKALRTIATDECELCINVACTGC 106
Db 67 CHHPALPDQLQPVCAQEAASFTFKALRTIATDECELCINVACTGC 111

RESULT 9

AAW18484

ID AAW18484 standard; peptide; 84 AA.

XX AAW18484;

XX 22-APR-1998 (first entry)

XX Human GCAP-II (89-112) chymotrypsin digested fragment 1.

XX Guanyl cyclase C activating peptide II; GCAP-II; insulinotropic;
KW diabetes; endocrine disorder; diagnosis; treatment; human.

XX Homo sapiens.

XX DE19543628-A1.

XX 28-MAY-1997.

XX 24-NOV-1995; 95DE-01043628.

XX 24-NOV-1995; 95DE-01043628.

XX (FORS/) FORSSMANN W.

XX Forsemann W, Kist A, Kruehoffer M, Meyer M, Pardigol A, Heine G;

XX WPI; 1997-290350/27.

XX New guanyl cyclase C activating peptide fragments - have insulinotropic
activity, useful for treating diabetes, etc.

XX Claim 3; Fig 3; 33pp; German.

XX Peptides AAW18484-W18487 represent fragments of the guanyl cyclase C
activating peptide, GCAP-II, obtained by digestion with chymotrypsin.
GCAP-II is involved in insulin secretion by pancreatic beta cells. This
peptide fragment could be used to which affects insulin secretion by the
beta cells treat pancreatic endocrine disorders, especially diabetes
mellitus type II, renal and intestinal disorders, disorders of the
respiratory, gastrointestinal and urogenital apparatus, disorders of the
cardiovascular and nervous systems, disorders of the integuments and
sense organs and diseases associated with GCAP II (89-112) deficiency.
This peptide can be used for treatment of electrolyte effects on bone
reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
-II (89-112) can be used to treat diseases associated with overproduction
of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
useful for diagnosis and treatment of the above disorders e.g. gene
therapy for diabetes

XX SQ Sequence 84 AA;

Query Match 55.5%; Score 304; DB 2; Length 84;
Best Local Similarity 67.5%; Pred. No. 1.1e-26;
Matches 56; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy 24 IKYHGFQVLESVKKLNELEEKQMSDPQOKSGLLPDVCYNPALPLDLQPVCAQEAAS 83
Db 1 IQYQGFQVLESMMKLSLEAQWAPSPRLQAOSSLPAVCHHPALPDQLQPVCAQEAASI 60

QY 84 FKALRTIATDECELCINVACTGC 106
 DB 61 FKTLRTIANDDCELCVNACTGC 83

RESULT 10
 AAW23232
 ID AAW23232 standard; peptide; 84 AA.
 AC AAW23232;
 XX
 XX 29-OCT-1997 (first entry)
 XX GCAP-II C-terminal fragment prepared by chymotrypsin.
 XX Human; guanylate cyclase; activating peptide; GCAP-II; cGMP;
 KW trans epithelial transport; treatment; kidney; intestinal; respiratory;
 KW urogenital; circulatory; nervous system; disorder; disease; endocrine;
 KW sensory; system; osteoporosis; dental; pancreas; diabetes; hypophysis;
 KW gastrointestinal tract; diarrhoea; gene therapy; probe;
 KW recombinant production; transgenic animal; antibody; immunoassay reagent.
 XX Homo sapiens.
 XX DE19528544-A1.
 XX 06-FEB-1997.
 XX 03-AUG-1995; 95DE-01028544.
 XX 03-AUG-1995; 95DE-01028544.
 XX (FORS/) FORSMANN W.
 XX Forssmann W;
 XX WPI; 1997-110032/11.
 XX Guanylate cyclase activating peptide II - increases cGMP formation, and
 PT controls transport of water and electrolytes across epithelial cells.
 XX Claim 3; Page 6; 15pp; German.

The present sequence is a carboxy-terminal fragment of the human
 CC guanylate cyclase activating peptide II (GCAP-II) precursor, prepared by
 CC endoproteolytic cleavage with chymotrypsin. GCAP-II increases cGMP
 CC formation, and is involved in the control of transepithelial water and
 CC electrolyte transport. GCAP-II can be used to treat a variety of kidney,
 CC intestinal, respiratory, urogenital, circulatory and nervous system
 CC disorders, diseases of the endocrine and sensory systems (e.g.
 CC osteoporosis, and dental disease), disorders of the pancreas (e.g.
 CC diabetes, and hypophysis) or the endocrine gastrointestinal tract and for
 CC the long term treatment of diarrhoea, without inducing an immune
 CC response. The GCAP-II cDNA can be used to treat the same conditions,
 CC clone the GCAP-II-encoding gene for use in gene therapy, as a
 CC transgenic animal creation. Antibodies raised against GCAP-II or
 CC as immunoassay reagents. GCAP-II, or a fragment, are administered at,
 CC e.g. 100-1200 microg/day by intravenous or intramuscular injection or 300
 CC -1200 microg/day subcutaneously. They may also be given orally,
 CC intranasally or by inhalation, in typical unit doses of 0.3-30 mg. GCAP-
 CC II was chemically synthesised, or isolated by chromatography from
 CC transformed eukaryotic or prokaryotic cells, or human blood. When T84
 CC cells were incubated with synthetic GCAP-II, generation of cGMP was
 CC increased in a dose dependent manner. GCAP-II influences cGMP production
 CC via a known receptor for heat stable enterotoxin. Other stomach,
 CC intestinal, pancreatic and liver cells also responded to GCAP-II, e.g.
 CC via changes in intracellular Ca²⁺ ion concentration

Sequence 84 AA;

Query Match 55.5%; Score 304; DB 2; Length 84;

Best Local Similarity 67.5%; Pred. No. 1.1e-26;
 Matches 56; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 24 IKYHGFQVLESVKLNLEEKQMSDPQOKSGLLPDVCYNPALPLDLPVCASQBAAST 83
 DB 1 IQVGFQVLESVKLNLEEKQMSDPQOKSGLLPDVCYNPALPLDLPVCASQBAAST 60
 QY 84 FKALRTIATDECELCINVACTGC 106
 DB 61 FKTLRTIANDDCELCVNACTGC 83

RESULT 11
 AAW18485
 ID AAW18485 standard; peptide; 81 AA.
 XX AC AAW18485;
 XX 22-APR-1998 (first entry)
 XX Human GCAP-II (89-112) chymotrypsin digested fragment 2.
 XX Guanylate cyclase C activating peptide II; GCAP-II; insulinotropic;
 KW diabetes; endocrine disorder; diagnosis; treatment; human.
 XX Homo sapiens.
 XX DE19543628-A1.
 XX 28-MAY-1997.
 XX 24-NOV-1995; 95DE-01043628.
 XX 24-NOV-1995; 95DE-01043628.
 XX (FORS/) FORSMANN W.
 XX Forssmann W, Kist A, Kruhoffer M, Meyer M, Pardigol A, Heine G;
 DR WPI; 1997-290350/27.
 XX New guanylate cyclase C activating peptide fragments - have insulinotropic
 PT activity, useful for treating diabetes, etc.
 XX Claim 3; Fig 3; 33pp; German.

Peptides AAW18484-W18487 represent fragments of the guanylate cyclase C
 CC activating peptide, GCAP-II, obtained by digestion with chymotrypsin.
 CC GCAP-II is involved in insulin secretion by pancreatic beta cells. This
 CC peptide fragment could be used to which affects insulin secretion by the
 CC beta cells treat pancreatic endocrine disorders, especially diabetes
 CC mellitus type II, renal and intestinal disorders, disorders of the
 CC respiratory, gastrointestinal and urogenital apparatus, disorders of the
 CC cardiovascular and nervous systems, disorders of the integuments and
 CC sense organs and diseases associated with GCAP II (89-112) deficiency.
 CC This peptide can be used for treatment of electrolyte effects on bone
 CC reconstruction (osteoporosis) or the dental apparatus. Antibodies to GCAP
 CC -II (89-112) can be used to treat diseases associated with overproduction
 CC of GCAP-II (89-112). Human GCAP-II (89-112) and GCAP I (99-15) cDNA are
 CC useful for diagnosis and treatment of the above disorders e.g. gene
 CC therapy for diabetes

Sequence 81 AA;

Query Match 53.3%; Score 292; DB 2; Length 81;
 Best Local Similarity 68.4%; Pred. No. 2.4e-25;
 Matches 54; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 28 GFQVLESVKLNLEEKQMSDPQOKSGLLPDVCYNPALPLDLPVCASQBAASTFKAL 87
 DB 2 GFRVLESVKLNLEEKQMSDPQOKSGLLPDVCYNPALPLDLPVCASQBAASTFKAL 61
 QY 88 RTIATDECELCINVACTGC 106

QY 30 QVQLESVKKLNELEEEKQMSDPQQQKSGLLPDVCYNPALPLDLQPVCASQEAASTFKALRT 89

Search completed: March 26, 2005, 16:44:28
Job time : 117.058 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2005, 16:37:18 ; Search time 96.4672 Seconds
(without alignments)
594.533 Million cell updates/sec

Title: US-10-775-481A-56

Perfect score: 579

Sequence: 1 MGRASGLLPVAVVLLLL.....RTIANDDELGVNACTGCL 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	100.0	112	1	GUAAU_HUMAN
2	452.5	78.2	113	1	GUAAU_PIG
3	404	69.8	111	1	GUAAU_CAVPO
4	368	63.6	106	1	GUAAU_MOUSE
5	368	63.6	106	2	Q9UQ03
6	362.5	62.6	107	2	Q8R5G8
7	356	61.5	106	1	GUAAU_RAT
8	285	49.2	109	1	GUAAU_DIDMA
9	167.5	28.9	109	1	GUAAU_PIG
10	162.5	28.1	115	1	GUAAU_HUMAN
11	161	27.8	108	2	Q98T10
12	161	27.8	108	2	Q7Z2S0
13	161	27.8	116	2	Q98T19
14	156	26.9	110	2	Q7Z2S1
15	153.5	26.5	109	2	Q7Z2S2
16	153.5	26.5	116	1	GUAAU_MOUSE
17	152	26.3	107	1	GUAAU_CAVPO
18	151	26.1	115	2	Q8R5G9
19	133	23.0	115	1	GUAAU_RAT
20	100	17.3	119	2	P70674
21	79.5	13.7	1168	2	Q7X5M9
22	77.5	13.4	353	2	Q9M6Q8
23	77	13.3	1010	2	Q8FGC0
24	77	13.3	3550	2	Q9JUN2
25	76.5	13.2	500	2	Q9FZ61
26	75	13.0	467	1	M3K8_RAT
27	74.5	12.9	393	2	Q56K77
28	74.5	12.9	533	2	Q9F1X4
29	74.5	12.9	937	1	R0R1_HUMAN
30	74	12.8	61	2	Q6VEG8
31	74	12.8	72	1	H5T3_ECOLI

32	74	12.8	467	1	M3K8_MOUSE	Q07174	mus musculus
33	74	12.8	677	2	Q7SB86	Q7AB86	neurospora
34	74	12.8	824	2	Q90778	Q90778	gallus gall
35	73.5	12.7	937	1	R0R1_MOUSE	Q92139	mus musculus
36	73.5	12.7	937	2	Q8BG10	Q8BG10	m mus muscu
37	73.5	12.7	937	2	Q8BNP9	Q8BNP9	mus musculus
38	73	12.6	457	2	Q7RLU1	Q7RLU1	giardia lam
39	72.5	12.5	792	2	Q7QWY7	Q7QWY7	giardia lam
40	72	12.4	467	1	M3K8_HUMAN	P41279	homo sapien
41	72	12.4	467	2	Q6FG25	Q6FG25	homo sapien
42	71.5	12.3	142	2	Q8WM60	Q8WM60	homo sapien
43	71.5	12.3	301	2	Q8TDQ0	Q8TDQ0	homo sapien
44	71.5	12.3	301	2	Q96K94	Q96K94	homo sapien
45	71	12.3	248	1	Y4UH_RHISN	Q53200	rhizobium s

ALIGNMENTS

RESULT 1
GUAAU_HUMAN
ID GUAAU_HUMAN STANDARD; PRT; 112 AA.
AC Q16661;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B)
DE (Guanylate cyclase C activating peptide II) (GCAP-II).
GN Name=GUCA2B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=96193705; PubMed=8605041; DOI=10.1006/bbrc.1996.0287;
RA Miyazato M., Nakazato M., Yamaguchi H., Date Y., Kojima M.,
RA Kangawa K., Matsuo H., Matsukura S.;
RT "Cloning and characterization of a cDNA encoding a precursor for human uroguanylin.";
RL Biochem. Biophys. Res. Commun. 219:644-648(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=96106424; PubMed=8519795; DOI=10.1016/0167-4838(95)00204-4;
RA Hill O., Cetin Y., Cieslak A., Maegert H.-J., Forssmann W.-G.;
RT "A new human guanylate cyclase-activating peptide (GCAP-II, uroguanylin): precursor cDNA and colonic expression.";
RL Biochim. Biophys. Acta 1253:146-149(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Maegert H.-J., Hill O., Forssmann W.-G.;
RT Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97422613; PubMed=9268639; DOI=10.1006/geno.1997.4808;
RA Miyazato M., Nakazato M., Matsukura S., Kangawa K., Matsuo H.;
RT "Genomic structure and chromosomal localization of human uroguanylin.";
RL Genomics 43:359-365(1997).
RN [5]
RP SEQUENCE OF 89-112, AND DISULFIDE BONDS.
RC TISSUE=Blood;
RX MEDLINE=96049550; PubMed=7589507; DOI=10.1016/0014-5793(95)01075-P;
RA Hess R., Kuhn M., Schulz-Knappe P., Raida M., Fuchs M., Klodt J.,
RA Adermann K., Kaever V., Cetin Y., Forssmann W.-G.;
RT "GCAP-II: isolation and characterization of the circulating form of human uroguanylin.";
RL FEBS Lett. 374:34-38(1995).
RN [6]
RP SEQUENCE OF 97-112, AND DISULFIDE BONDS.

MEDLINE=94189775; PubMed=8141334;
 Kita T., Smith C.E., Fok K.F., Duffin K.L., Moore W.M.,
 Karabatos P.J., Kachur J.F., Hamra F.K., Pichorodeckj N.V.,
 Forte L.R., Currie M.G.;
 "Characterization of human uroguanylin: a member of the guanylin
 peptide family";
 Am. J. Physiol. 266:F342-F348(1994).
 [7]
 STRUCTURE BY NMR OF 97-112.
 MEDLINE=98445220; PubMed=9774236;
 Marx U.C., Klott J., Meyer M., Gerlach H., Roesch P., Forssmann W.-G.,
 Adermann K.;
 "One peptide, two topologies: structure and interconversion dynamics
 of human uroguanylin isomers";
 J. Pept. Res. 52:229-240(1998).
 -!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
 stimulates this enzyme through the same receptor binding region as
 the heat-stable enterotoxins. May be a potent physiological
 regulator of intestinal fluid and electrolyte transport. May be an
 autocrine/paracrine regulator of intestinal salt and water
 transport.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- TISSUE SPECIFICITY: Stomach and intestine.
 -!- SIMILARITY: Belongs to the guanylin family.

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 or send an email to license@isb-sib.ch).

 EMBL; U34279; AAC50416.1; -;
 EMBL; Z50753; CAA90629.1; -;
 EMBL; Z70295; CAA94311.1; -;
 EMBL; U55058; AAC51729.1; -;
 PIR; JC4651; JC4651.
 PDB; 1UYA; NMR; @=97-112.
 PDB; 1UYB; NMR; @=97-112.
 Genew; HGNC:4683; GUCR2B.
 MIM; 601271; -;
 GO; GO:0008048; F:calcium sensitive guanylate cyclase activat. .; TAS.
 GO; GO:0007588; P:excretion; TAS.
 InterPro; IPR000879; Guanylin.
 Pfam; PF02058; Guanylin; 1.
 PIRSF; PIRSF001849; Guanylin; 1.
 PRINTS; PR00774; GUANYLIN.
 ProDom; PD005588; Guanylin; 1.
 3D-structure; Direct protein sequencing; Signal.
 SIGNAL 1 26 Potential.
 PROPEL 27 88
 PROPEL 89 112 GCAP-II.
 PEPTIDE 97 112 Uroguanylin.
 PEPTIDE 97 112 Potential.
 DISULFID 67 80
 DISULFID 100 108
 DISULFID 103 111
 TURN 109 110
 SEQUENCE 112 AA; 12069 MW; AA3030BC3D4EE412 CRC64;

 Query Match 100.0%; Score 579; DB 1; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5.1e-51;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MCGRAASGLLPGVAVVLLLLQSTQSVYQYQGFVQLSESMKKLSDLQAWAPSPRLQ 60
 DB 1 MCGRAASGLLPGVAVVLLLLQSTQSVYQYQGFVQLSESMKKLSDLQAWAPSPRLQ 60

 QY 61 SLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTIANDCELQVNVACTGCL 112
 DB 61 SLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTIANDCELQVNVACTGCL 112

```

DE Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B).
GN Name=GUCA2B;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Kruhoffer M., Meyer M.F., Schlatter E., Kaempf U., Cetin Y.,
RA Forssmann W.-G.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
CC stimulates this enzyme through the same receptor binding region as
CC the heat-stable enterotoxins. May be a potent physiological
CC regulator of intestinal fluid and electrolyte transport. May be an
CC autocrine/paracrine regulator of intestinal salt and water
CC transport.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the guanylin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; Z74738; CRA98994.1; -.
DR HSP; Q16661; IUYA.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PIRSF; PIRSF001849; Guanylin; 1.
DR PRINTS; PR00774; GUANYLIN.
DR ProDom; PD005588; Guanylin; 1.
KW Signal.
FT SIGNAL 1 26 Potential.
FT PROPEP 27 96
FT PEPTIDE 97 111 Uroguanylin.
FT DISULFID 67 80 Potential.
FT DISULFID 100 108 By similarity.
FT DISULFID 103 111 By similarity.
SQ SEQUENCE 111 AA; 12125 MW; 7C3366A721FE0411 CRC64;

Query Match 69.8%; Score 404; DB 1; Length 111;
Best Local Similarity 70.3%; Pred. No. 3.1e-33;
Matches 78; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MGCRAAGLLPGVAVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQ 60
Db 1 MGSRTLLGHSVLAVVLLLLQSTQSDVIKYQGVQVLESVKKLKALEEQWVSPRLQAQ 60

Qy 61 SLLPAVCHHPALPDQLQPVCAQSEASSIFKTLRTIANDCELCVNACTGC 111
Db 61 DPQPAVCHHPALPDQLQPTCSQEAASILQALRTMDNDECELCVNIACTGC 111

RESULT 4
GUAN_MOUSE STANDARD; PRT; 106 AA.
AC O09051;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B).
GN Name=Guca2b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97434109; PubMed=9287995;
RA Whitaker T.L., Witte D.P., Scott M.C., Cohen M.B.;
RT "Uroguanylin and guanylin: distinct but overlapping patterns of
RT messenger RNA expression in mouse intestine.";
RL Gastroenterology 113:1000-1006(1997).
RN [2]
RP REVISION TO 17.
RA Sanford L.P., Cohen M.B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
CC stimulates this enzyme through the same receptor binding region as
CC the heat-stable enterotoxins. May be a potent physiological
CC regulator of intestinal fluid and electrolyte transport. May be an
CC autocrine/paracrine regulator of intestinal salt and water
CC transport (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Localized predominantly in intestinal villi
CC and the corticomedullary junction of the kidney.
CC -!- SIMILARITY: Belongs to the guanylin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U95182; AAB82750.2; -.
DR EMBL; U90727; AAB53314.1; -.
DR HSP; Q16661; IUYA.
DR MGD; MG1:1270851; Guca2b.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PRINTS; PR00774; GUANYLIN.
DR ProDom; PD005588; Guanylin; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 91
FT PEPTIDE 92 106 Uroguanylin.
FT DISULFID 62 75 Potential.
FT DISULFID 95 103 By similarity.
FT DISULFID 98 106 By similarity.
FT CONFLICT 17 17 Q -> R (in Ref. 1; AAB53314).
SQ SEQUENCE 106 AA; 11627 MW; 30FF1CCE9D293DA8 CRC64;

Query Match 63.6%; Score 368; DB 1; Length 106;
Best Local Similarity 71.4%; Pred. No. 1.4e-29;
Matches 70; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 14 AVVLLLLQSTQSVYIQGFRVQLESMMKLSLEAQWAPSPRLQAQSLPVCVHPALP 73
Db 9 AVVLLLLQSAQGVYIKYHGFQVQLESVKKLEKEKEMSNPQPRRSGLLPVCVHPALP 68

Qy 74 QDLQPVCAQSEASSIFKTLRTIANDCELCVNACTGC 111
Db 69 LDLQPVCAQSEASSIFKTLRTIANDCELCVNACTGC 106

RESULT 5
Q9QUQ3 PRELIMINARY; PRT; 106 AA.
ID Q9QUQ3
AC Q9QUQ3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Uroguanylin (Guca2b protein) (Mus musculus adult male kidney cDNA,
DE RIKEN full-length enriched library, clone:0610009B03 product:guanylate
DE cyclase activator 2b (retina), full insert sequence).
GN Name=Guca2b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazato M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N, TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klugner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N, TISSUE=Kidney;
RX Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Miyazato M.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TISSUE=Kidney;
RX The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Hashiwa K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TISSUE=Kidney;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Konda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006668; AAD09311.1; -
DR EMBL; BC024373; AAD09215.1; -
DR EMBL; U67800; AAD09215.1; -
DR EMBL; AK002364; BAB22042.1; -
DR HSSP; Q16661; IUYA.
DR MGD; MGI:1270851; Guca2b.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006182; P:cGMP biosynthesis; IMP.
DR GO; GO:0007589; P:fluid secretion; IMP.
DR GO; GO:0045776; P:negative regulation of blood pressure; IMP.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PIRSF; PIRSF001849; Guanylin; 1.
DR PRINTS; PD00774; GUANYLIN.
DR ProDom; PD005588; Guanylin; 1.
DR SEQUENCE 106 AA; 11627 MW; 30FF1CCE9D293DA8 CRC64;
Query Match 63.6%; Score 368; DB 2; Length 106;
Best Local Similarity 71.4%; Pred. No. 1.4e-29;
Matches 70; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
QY 14 AVVLLLLQSTQSVTYQGFVQLSEMKKLSLEAQAQSPRLQAQSLLPVCHHPALP 73
Db 9 AVVLLLLQSAQGVYKYHGFQVQLSEVKKLEKEKMSNFPRRSGLLPVCNHPALP 68
QY 74 QLOPVCASQEAASSIFKTLRTTANDDCELCVNACTGC 111
Db 69 LDLPQVCASQEAASFTKALRTIATDECELINACTGC 106
RESULT 6
Q8R5G8 PRELIMINARY; PRT; 107 AA.
ID Q8R5G8;
AC Q8R5G8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Droganylin.
OS Notoxys alexis (Spinifex hopping mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Notomys.
OX NCBI_TaxID=184396;
RN [1]
RP SEQUENCE FROM N.A.
RA Donald J.A., Bartolo R.C.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469496; AAL77417.1; -
DR HSSP; Q16661; IUYA.

GO; GO:0008047; F:enzyme activator activity; IEA.
 InterPro; IPR000879; Guanylin.
 Pfam; PF02058; Guanylin; 1.
 PIRSF; PIRSF001849; Guanylin; 1.
 PRINTS; PR00774; GUANYLIN.
 ProDom; PD005588; Guanylin; 1.
 SEQUENCE 107 AA; 11618 MW; 735110CAC60DA97 CRC64;

Query Match 62.6%; Score 362.5; DB 2; Length 107;
 Best Local Similarity 67.9%; Pred. No. 5e-29;
 Matches 72; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

Qy 7 SGLPGVAVVLLLLQSTQSVYIQGFRVQLESKMLSDLEAQWASPRLQAS-LLPA 65
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 2 SGSQWAAVLLVLSQAQGYIYKHGFQVLESVKLSELEKQMSPOLKSGLLPD 61
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 66 VCHHPALPDLPQVCASQEAASSIFKTLRTIANDCELCNVACTGC 111
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 62 VCHHPALPDLPQVCASQEAASSIFKTLRTIANDCELCNVACTGC 107
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
 GUAAU RAT STANDARD; PRT; 106 AA.
 ID GUAAU RAT
 AC P70666;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B).
 GN Name=Guca2b;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 92-106.
 RC STRAIN=Sprague-Dawley;
 RA MEDLINE=97248740; PubMed=9094754; DOI=10.1016/S0167-0115(96)02103-9;
 RX Li Z., Perkins A.G., Peters M.F., Campa M.J., Goy M.F.;
 RT "Purification, cDNA sequence, and tissue distribution of rat
 uroguanylin";
 RL Regul. Pept. 68:45-56(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97131589; PubMed=89771100; DOI=10.1016/S0014-5793(96)01235-5;
 RX Miyazato M., Nakazato M., Matukura S., Kangawa K., Matsuo H.;
 RT "Uroguanylin gene expression in the alimentary tract and extra-
 gastrointestinal tissues";
 RL FEBS Lett. 398:170-174(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Small intestine;
 RX MEDLINE=97319300; PubMed=9176203;
 RA Blanchard R.K., Cousins R.J.;
 RT "Upregulation of rat intestinal uroguanylin mRNA by dietary zinc
 restriction";
 RL Am. J. Physiol. 272:G972-G978(1997).
 CC -1- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
 stimulates this enzyme through the same receptor binding region as
 the heat-stable enterotoxins. May be a potent physiological
 regulator of intestinal fluid and electrolyte transport. May be an
 autocrine/paracrine regulator of intestinal salt and water
 transport.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed not only in the gastrointestinal
 tract but also in the lung, pancreas and kidney.
 CC -1- SIMILARITY: Belongs to the guanylin family.

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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U73898; AAB18331.1; -;
 CC EMBL; U41322; AAB18760.1; -;
 CC EMBL; U75186; AAB61209.1; -;
 CC HSSP; Q16661; IUYA.
 CC RGD; 620044; Guca2b.
 CC InterPro; IPR000879; Guanylin.
 CC Pfam; PF02058; Guanylin; 1.
 CC PIRSF; PIRSF001849; Guanylin; 1.
 CC PRINTS; PR00774; GUANYLIN.
 CC ProDom; PD005588; Guanylin; 1.
 KW Direct protein sequencing; Signal.
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 91
 FT PEPTIDE 92 106 Uroguanylin.
 FT DISULFID 62 75 Potential.
 FT DISULFID 95 103 By similarity.
 FT DISULFID 98 106 By similarity.
 SQ SEQUENCE 106 AA; 11573 MW; 9PB5P8A9B1DD077 CRC64;

Query Match 61.5%; Score 356; DB 1; Length 106;
 Best Local Similarity 65.7%; Pred. No. 2.2e-28;
 Matches 69; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy 7 SGLPGVAVVLLLLQSTQSVYIQGFRVQLESKMLSDLEAQWASPRLQASLLPAV 66
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 2 SGSQWAAVLLVLSQAQGYIYKHGFQVLESVKLSELEKQMSDPQQKSGLLPDV 61
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 67 CHHPALPDLPQVCASQEAASSIFKTLRTIANDCELCNVACTGC 111
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 62 CYNPALPDLPQVCASQEAASSIFKTLRTIANDCELCNVACTGC 106
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
 GUAAU DIDMA STANDARD; PRT; 109 AA.
 ID GUAAU DIDMA
 AC Q28358;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B).
 GN Name=GUCA2B;
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=96193673; PubMed=8605009; DOI=10.1006/bbrc.1996.0255;
 RA Fan X., Hamra F.K., Freeman R.H., Eber S.L., Krause W.J., Lim R.W.,
 Pace V.M., Currie M.G., Forte L.R.;
 RT "Uroguanylin: Cloning of preproguanylin cDNA, mRNA expression in
 the intestine and heart and isolation of uroguanylin and
 proguanylin from plasma";
 RL Biochem. Biophys. Res. Commun. 219:457-462(1996).
 RN [2]
 RP SEQUENCE OF 95-109.
 RC TISSUE=Urine;
 RX MEDLINE=94068421; PubMed=7902563;
 RA Hamra F.K., Forte L.R., Eber S.L., Pidhoreckij N.V., Krause W.J.,
 Freeman R.H., Chin D.T., Tompkins J.A., Fok K.F., Smith C.E.,
 Duffin K.L., Siegel N.R., Currie M.G.;
 RT "Uroguanylin: structure and activity of a second endogenous peptide
 that stimulates intestinal guanylate cyclase";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10464-10468(1993).
 CC -1- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It
 stimulates this enzyme through the same receptor binding region as
 the heat-stable enterotoxins. May be a potent physiological
 regulator of intestinal fluid and electrolyte transport. May be an
 autocrine/paracrine regulator of intestinal salt and water

transport.
 -1- SUBCELLULAR LOCATION: Secreted.
 -1- TISSUE SPECIFICITY: Small and large intestine and atria and ventricles of heart. Both uroguanylin and prouroguanylin are found in plasma.
 -1- SIMILARITY: Belongs to the guanylin family.

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 EMBL; U49353; AAB00553.1; -;
 DR HSPSP; Q16661; IUYA.
 DR InterPro; IPR000879; Guanylin.
 DR Pfam; PF02058; Guanylin; 1.
 DR PIRSF; PIRSF001849; Guanylin; 1.
 DR PRINTS; PR00774; GUANYLIN.
 DR ProDom; PD005588; Guanylin; 1.
 KW Direct protein sequencing; Signal.
 FT SIGNAL 1 23 Potential.
 FT PROPEP 24 94
 FT PEPTIDE 95 109 Uroguanylin.
 FT DISULFID 65 78 Potential.
 FT DISULFID 98 106 By similarity.
 FT DISULFID 101 109 By similarity.
 SQ SEQUENCE 109 AA; 12040 MW; AE948E210CA3AE7A CRC64;

 Query Match 49.2%; Score 285; DB 1; Length 109;
 Best Local Similarity 54.8%; Pred. No. 3.8e-21;
 Matches 57; Conservative 21; Mismatches 24; Indels 2; Gaps 2;

 QY 10 LP-GVAVLLLLQSTQSVYIQGFRVQLSEMKKLSL-LEAQWAPSRLQAQSLPAVC 67
 DB 6 LPVAVAMLLVLAQNTQSVYIQEGFQKLSVKLDELLEQPRSFRRMGTRQDPFSLC 65
 QY 68 HHPLPDLPQVCASQASISFKTLRTIANDCELQVNVACTGC 111
 DB 66 SDPALPSDLPQVCNSQAANIFALRSIQEDCELQVNVACTGC 109

 RESULT 9
 GUAN_PIG STANDARD; PRT; 109 AA.
 AC P79897;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Guanylin precursor (Guanylate cyclase activator 2A).
 GN Name=GUCA2A; Synonyms=GUCA2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Jejunum;
 RX MEDLINE=99268812; PubMed=10334930; DOI=10.1006/bbr.1999.0719;
 RA Maegert H.J., Hill O., Zucht H.D., Martin S., Meyer M.,
 RA Forsemann W.-G., Adermann K.;
 RT "Porcine guanylin and uroguanylin: cDNA sequences, deduced amino acid sequences, and biological activity of the chemically synthesized peptides";
 RL Biochem. Biophys. Res. Commun. 259:141-148(1999).
 CC -1- FUNCTION: Endogenous activator of intestinal guanylate cyclase. It stimulates this enzyme through the same receptor binding region as the heat-stable enterotoxins.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the guanylin family.

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 EMBL; Z73607; CAA97974.1; -;
 DR HSPSP; Q02747; IGNA.
 DR InterPro; IPR000879; Guanylin.
 DR Pfam; PF02058; Guanylin; 1.
 DR PIRSF; PIRSF001849; Guanylin; 1.
 DR PRINTS; PR00774; GUANYLIN.
 DR ProDom; PD005588; Guanylin; 1.
 KW Signal.
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 94
 FT PEPTIDE 95 109 Guanylin.
 FT DISULFID 98 106 By similarity.
 FT DISULFID 101 109 By similarity.
 SQ SEQUENCE 109 AA; 11938 MW; 6368BD1FB0B07A7A CRC64;

 Query Match 28.9%; Score 167.5; DB 1; Length 109;
 Best Local Similarity 42.0%; Pred. No. 3.4e-09;
 Matches 34; Conservative 12; Mismatches 32; Indels 3; Gaps 2;

 QY 34 FRVQLSEMKKLSL-LEAQWAPSRLQAQSLPAVCCHHPALPDLPQVCASQASISFKTL 92
 DB 29 FFSLSLVKLLDLQELQKPRNRLDGLIIPVLNPKFPPELPIQCKPNAEILRL 88
 QY 93 RTIAND--DCELQVNVACTGC 111
 DB 89 ETIAQDPSTCEICAYACAGC 109

 RESULT 10
 GUAN_HUMAN STANDARD; PRT; 115 AA.
 AC Q02747;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Guanylin precursor (Guanylate cyclase activator 2A) (Guanylate cyclase activating protein 1) (Gap-1).
 GN Name=GUCA2A; Synonyms=GUCA2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Duodenum;
 RX MEDLINE=930111964; PubMed=1327879; DOI=10.1016/0014-5793(92)81387-2;
 RA Wiegand R.C., Kato J., Huang M.D., Fok K.F., Kachur J.F., Currie M.G.;
 RT "Human guanylin: cDNA isolation, structure, and activity";
 RL FEBS Lett. 311:150-154(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ileum;
 RX MEDLINE=93028409; PubMed=1409606;
 RA de Sauvage F.J., Keshav S., Kuang W.J., Gillett N., Henzel W.,
 RA Goeddel D.V.;
 RT "Precursor structure, expression, and tissue distribution of human guanylin";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9089-9093(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95192989; PubMed=7892222;
 RA Hill O., Kuhn M., Zucht H.D., Cetin Y., Kulaksiz H., Adermann K.,
 RA Klock G., Reckemmer G., Forsemann W.-G., Magert H.J.;
 RT "Analysis of the human guanylin gene and the processing and cellular

[illegible]

RT eels: possible osmoregulatory hormones in intestine and kidney. ";
RL J. Biol. Chem. 278:22726-22733 (2003).
DR EMBL; AB080642; BAC76011.1; -
DR HSSP; Q02747; 108R.
DR GO; GO:0008047; F:enzyme activator activity; IEA.
DR InterPro; IPR006058; 2Fe2S fd BS.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PIRSF; PIRSF001849; Guanylin; 1.
DR PRINTS; PR00774; GUANYLIN.
DR ProDom; PD005588; Guanylin; 1.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; UNKNOWN 1.
SQ SEQUENCE 108 AA; 11584 MW; 8A3B6D490E7C858D CRC64;

Query Match 27.8%; Score 161; DB 2; Length 108;
Best Local Similarity 39.4%; Pred. No. 1.5e-08;
Matches 43; Conservative 13; Mismatches 39; Indels 14; Gaps 4;

QY 14 AVVLLLL-----LSTQSVYIQYQGRVQLSEMKKLSDLAEQWAPS-----PRLOAQSLLLPA 65
DB 4 AVVLLLLAFCLQESQGVWMDGLSPLEAVKVLKHLGANTMTSTPPHNLGSH-----A 59

QY 66 VCHHPALPDQLQPVCAQSEASSIFKTLRTIAN--DCELCVNVACTGCL 112
DB 60 VCSNPHLPFAEFLPVCEREGASALFNRLVDIITPPDPCEICANAACTGCL 108

RESULT 13
Q98TH9 ID Q98TH9 PRELIMINARY; PRT; 116 AA.
AC Q98TH9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Guanylin.
GN Name=GUCAZII;
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7936;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21139737; PubMed=11243845; DOI=10.1006/bbrc.2001.4485;
RA Comrie M.M., Cutler C.P., Cramb G.;
RT "Cloning and Expression of Guanylin from the European eel (Anguilla anguilla).";
RL Biochem. Biophys. Res. Commun. 281:1078-1085 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Comrie M.M.;
RL Thesis (2000), Department of School of Biology, University of St Andrews, St Andrews, United Kingdom.
DR EMBL; AJ301673; CAC35449.1; -
DR PIR; JC7620; JC7620.
DR HSSP; Q02747; 108R.
DR GO; GO:0008047; F:enzyme activator activity; IEA.
DR InterPro; IPR006058; 2Fe2S fd BS.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PIRSF; PIRSF001849; Guanylin; 1.
DR PRINTS; PR00774; GUANYLIN.
DR ProDom; PD005588; Guanylin; 1.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; UNKNOWN 1.
SQ SEQUENCE 116 AA; 12547 MW; 38B3DAF0AC0B39E0 CRC64;

Query Match 27.8%; Score 161; DB 2; Length 116;
Best Local Similarity 39.4%; Pred. No. 1.7e-08;
Matches 43; Conservative 13; Mismatches 39; Indels 14; Gaps 4;

QY 14 AVVLLLL-----LSTQSVYIQYQGRVQLSEMKKLSDLAEQWAPS-----PRLOAQSLLLPA 65
DB 12 AVVLLLLAFCLQESQGVWMDGLSPLEAVKVLKHLGANTMTSTPPHNLGSH-----A 67

QY 66 VCHHPALPDQLQPVCAQSEASSIFKTLRTIAN--DCELCVNVACTGCL 112
DB 68 VCSNPHLPFAEFLPVCEREGASALFNRLVDIITPPDPCEICANAACTGCL 116

RESULT 14
Q7ZS21 ID Q7ZS21 PRELIMINARY; PRT; 110 AA.
AC Q7ZS21
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Preprorenoguanilin.
GN Name=renoguanilin;
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Intestine;
RC MEDLINE=22692502; PubMed=12684514; DOI=10.1074/jbc.M303111200;
RA Yuge S., Inoue K., Hyodo S., Takei Y.;
RT "A novel guanylin family (guanylin, uroguanylin, and renoguanilin) in eels: possible osmoregulatory hormones in intestine and kidney.";
RL J. Biol. Chem. 278:22726-22733 (2003).
DR EMBL; AB080641; BAC76010.1; -
DR HSSP; Q02747; 108R.
DR GO; GO:0008047; F:enzyme activator activity; IEA.
DR InterPro; IPR006058; 2Fe2S fd BS.
DR InterPro; IPR000879; Guanylin.
DR Pfam; PF02058; Guanylin; 1.
DR PIRSF; PIRSF001849; Guanylin; 1.
DR PRINTS; PR00774; GUANYLIN.
DR ProDom; PD005588; Guanylin; 1.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; UNKNOWN 1.
SQ SEQUENCE 110 AA; 11646 MW; B161A03A913894F9 CRC64;

Query Match 26.9%; Score 156; DB 2; Length 110;
Best Local Similarity 37.1%; Pred. No. 5e-08;
Matches 39; Conservative 21; Mismatches 39; Indels 6; Gaps 3;

QY 13 VAVVLLLLQLSTQSVYIQYQGRVQLSEMKKLSDL---EAQWAPSRLQAOQLLPAVCHH 69
DB 7 INTLLVALALVTEAVQVEEGSFPLDVAVKLEELMGVDMTVKQSPRL-AKTSTTAVCTN 65

QY 70 PALPDQLQPVCAQSEASSIFKTLRTIA--NDDCELCVNVACTGCL 112
DB 66 PDLPAVFLPLCKSKGANSFRLGFAARADLCEICAFNACTGCL 110

RESULT 15
Q7ZS22 ID Q7ZS22 PRELIMINARY; PRT; 109 AA.
AC Q7ZS22
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Preproguanylin.
GN Name=guanylin;
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Intestine;
RC MEDLINE=22692502; PubMed=12684514; DOI=10.1074/jbc.M303111200;
RA Yuge S., Inoue K., Hyodo S., Takei Y.;
RT "A novel guanylin family (guanylin, uroguanylin, and renoguanilin) in

RT eels: possible osmoregulatory hormones in intestine and kidney.":

RL J. Biol. Chem. 278:22726-22733(2003).

DR EMBL; AB080640; BAC76009.1; -.

DR HSSP; Q02747; 108R.

DR GO; GO:0008047; F:enzyme activator activity; IEA.

DR InterPro; IPR006058; 2Fe2S_fd_BS.

DR InterPro; IPR000879; Guanylin.

DR Pfam; PF02058; Guanylin; 1.

DR PRINTS; PR00774; GUANYLIN.

DR PRODom; PD005588; Guanylin; 1.

DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN 1.

SQ SEQUENCE 109 AA; 11773 MW; A25C40D085A556C7 CRC64;

Query Match

Best Local Similarity 26.5%; Score 153.5; DB 2; Length 109;

Matches 37; Conservative 21; Mismatches 37; Indels 9; Gaps 4;

Qy 13 VAVVLLILLQSTQSVYIQGFRVQLESMMKLSDL---EAQWAPSPRLQAQSLLPVACHH 69

Db 10 LALAVSLLCDVQ---VKEREFTFSLESVRQLKLDMSDLAGKESPRL-AKTSTAIVCND 65

Qy 70 PALPDQLQPVCAQSEASSIPKTLRTIAN--DDCELCVNVACTGC 111

Db 66 PGLPEEFLPLCQSEGAGSLARLAFIGNNYDECEICWFACCTGC 109

Search completed: March 26, 2005, 16:48:36

Job time : 97.4672 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:44:35 ; Search time 5.89416 Seconds
(without alignments)
187.395 Million cell updates/sec

Title: US-10-775-481A-2

Perfect score: 127

Sequence: 1 NTFYCCCLCCNPACAGCY 19

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 260697 seqs, 58133403 residues

Total number of hits satisfying chosen parameters: 260697

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New.*

1: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US12_NEW_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	95.3	18	6	US-10-934-728-24
2	60	47.2	3398	1	PCT-US05-03560-6
3	59	46.5	424	6	US-10-450-763-42525
4	58	45.7	16	7	US-11-066-697-1249
5	56	44.1	690	6	US-10-938-061-106
6	56	44.1	690	6	US-10-936-626-106
7	55	43.3	98	6	US-10-489-448-3215
8	55	43.3	154	6	US-10-489-448-1582
9	54	42.5	1071	1	PCT-US05-05406-6
10	54	42.5	1071	7	US-11-060-291-6
11	54	42.5	1123	6	US-10-287-436A-285
12	53.5	42.1	103	6	US-10-489-448-1704
13	53	41.7	381	6	US-10-287-436A-258
14	53	41.7	623	6	US-10-287-436A-243
15	53	41.7	4440	6	US-10-184-644-525
16	53	41.7	4440	6	US-10-192-007-525
17	52.5	41.3	152	8	US-60-655-875-169174
18	52.5	41.3	158	8	US-60-655-875-163386
19	52.5	41.3	317	8	US-60-643-717-15143
20	52.5	41.3	1501	5	US-09-857-581B-16
21	52	40.9	1300	6	US-10-184-644-269
22	52	40.9	1300	6	US-10-192-007-269
23	52	40.9	1435	6	US-10-184-644-581
24	52	40.9	1435	6	US-10-192-007-581
25	51.5	40.6	320	8	US-60-643-717-15714

26	51.5	40.6	321	8	US-60-643-717-15702	Sequence 15702, A
27	51.5	40.6	327	8	US-60-643-717-15738	Sequence 15738, A
28	51.5	40.6	328	8	US-60-643-717-15729	Sequence 15729, A
29	51.5	40.6	328	8	US-60-643-717-15736	Sequence 15736, A
30	51	40.2	215	6	US-10-450-763-56787	Sequence 56787, A
31	51	40.2	309	1	PCT-US04-17965-1363	Sequence 1363, Ap
32	51	40.2	309	1	PCT-US04-17965B-1363	Sequence 1363, Ap
33	51	40.2	328	8	US-60-643-717-16005	Sequence 16005, A
34	51	40.2	1743	6	US-10-184-644-451	Sequence 451, App
35	51	40.2	1743	6	US-10-192-007-451	Sequence 451, App
36	50.5	39.8	460	6	US-10-287-436A-274	Sequence 274, App
37	50.5	39.8	1588	6	US-10-818-210A-2	Sequence 2, Appl
38	50	39.4	12	6	US-10-934-728-22	Sequence 22, Appl
39	50	39.4	15	6	US-10-934-728-25	Sequence 25, Appl
40	50	39.4	15	7	US-11-066-697-1247	Sequence 1247, Ap
41	50	39.4	15	7	US-11-066-697-1248	Sequence 1248, Ap
42	50	39.4	330	6	US-10-287-436A-232	Sequence 232, App
43	50	39.4	505	8	US-60-643-717-611	Sequence 611, App
44	50	39.4	505	8	US-60-643-717-17547	Sequence 17547, A
45	50	39.4	508	6	US-10-489-448-1646	Sequence 1646, Ap

ALIGNMENTS

RESULT 1
US-10-934-728-24
; Sequence 24, Application US/10934728
; GENERAL INFORMATION:
; APPLICANT: Balloul, Jean Marc
; APPLICANT: Paul, Stephane
; APPLICANT: Geist, Michel
; APPLICANT: Silvestre, Nathalie
; APPLICANT: Erbs, Philippe
; TITLE OF INVENTION: Foxvirus With Targeted Infection Specificity
; FILE REFERENCE: 032751-115
; CURRENT APPLICATION NUMBER: US/10/934, 728
; CURRENT FILING DATE: 2004-09-07
; PRIOR APPLICATION NUMBER: US 09/832,899
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: US 60/246,080
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: EP 0040109.7
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: EP 01440009.7
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sta ligand
US-10-934-728-24

Query Match 95.3% ; Score 121; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NTFYCCCLCCNPACAGCY 19
|||||
Db 1 NTFYCCCLCCNPACAGCY 18
|||||

RESULT 2
PCT-US05-03560-6

; Sequence 6, Application PC/TUS0503560
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: ITPKS AS SMODIFIERS OF THE IGFR PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX05-004C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03560

; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,837
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; TYPE: PRT
; LENGTH: 3398
; ORGANISM: Homo sapiens
PCT-US05-03560--6

Query Match 47.2%; Score 60; DB 1; Length 3398;
Best Local Similarity 61.5%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CCELCNCPACAGC 18
||| ||| ||| |||
DB 2463 CCTCCTGTGACG 2475

RESULT 3

US-10-450-763-42525
; Sequence 42525, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 03/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 42525
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-42525

Query Match 46.5%; Score 59; DB 6; Length 424;
Best Local Similarity 52.6%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 NNTFYCCELCNCPACAGCY 19
| | | | | | | | | |
DB 187 NGVFSCSILCLNPNARGCY 205

RESULT 4

US-11-066-697-1249
; Sequence 1249, Application US/11066697
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Eridon, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 50086202301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15

; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1249
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1249

Query Match 45.7%; Score 58; DB 7; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CELCCNPACAGC 18
||| ||| ||| |||
DB 4 CELCVNACTGC 15

RESULT 5

US-10-938-061-106
; Sequence 106, Application US/10938061
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; APPLICANT: Sakanaka, Chie
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Reed Chae J.
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1P1B
; CURRENT APPLICATION NUMBER: US/10/938,061
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 10/872,991
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/872,972
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/241,220
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/557,116
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/598,899
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 106
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-061-106

Query Match 44.1%; Score 56; DB 6; Length 690;
Best Local Similarity 50.0%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 YCCELCCNPACAGC 18
Db 620 YCCRVCCACCLLC 633

RESULT 6

US-10-936-626-106

; Sequence 106, Application US/10936626
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1P1
; CURRENT APPLICATION NUMBER: US/10/936,626
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: US 10/872,991
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/872,972
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/241,220
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/557,116
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/598,899
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 106
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-936-626-106

Query Match 44.1%; Score 56; DB 6; Length 690;
Best Local Similarity 50.0%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 YCCELCCNPACAGC 18
Db 620 YCCRVCCACCLLC 633

RESULT 7

US-10-489-448-3215

; Sequence 3215, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika

; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yungqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pcfl_genes Version 6.0
; SEQ ID NO 3215
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(98)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for
US-10-489-448-3215

Query Match 43.3%; Score 55; DB 6; Length 98;
Best Local Similarity 70.0%; Pred. No. 1.4;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCELCNCPAC 15
Db 16 CCQPCCRPAC 25

RESULT 8

US-10-489-448-1582
; Sequence 1582, Application US/10489448
; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yungqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana

APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 810CIP PCT
CURRENT APPLICATION NUMBER: US/10/489,448
CURRENT FILING DATE: 1004-03-10
PRIOR APPLICATION NUMBER: US 60/324,631
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3476
SOFTWARE: PCT_Fl_genes Version 6.0
SEQ ID NO 1562
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapiens
US-10-489-448-1582

Query Match 43.3%; Score 55; DB 6; Length 154;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCELCNCPAC 15
DB 125 CCQPCCRPAC 134

RESULT 9
PCT-US05-05406-6
Sequence 6, Application PC/TUS0505406
GENERAL INFORMATION:
APPLICANT: Olsen, Byron
TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the
FILE REFERENCE: GTC-223 PCT
CURRENT APPLICATION NUMBER: PCT/US05/05406
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: 60/545,790
PRIOR FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 1071
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US05-05406-6

Query Match 42.5%; Score 54; DB 1; Length 1071;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CCELCNCPAC 18
DB 261 CCGACCTCTCGGC 273

RESULT 10
US-11-060-291-6
Sequence 6, Application US/11060291
GENERAL INFORMATION:
APPLICANT: Olsen, Byron
TITLE OF INVENTION: Treatment of Obesity and Diabetes
FILE REFERENCE: GTC-223
CURRENT APPLICATION NUMBER: US/11/060,291
CURRENT FILING DATE: 2005-02-17
PRIOR APPLICATION NUMBER: 60/545,790
PRIOR FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 1071
TYPE: PRT
ORGANISM: Homo sapiens
US-11-060-291-6

Query Match 42.5%; Score 54; DB 7; Length 1071;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CCELCNCPAC 18
DB 261 CCGACCTCTCGGC 273

RESULT 11
US-10-287-436A-285
Sequence 285, Application US/10287436A
GENERAL INFORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: RHEUMATOID ARTHRITIS
FILE REFERENCE: 10872-514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 285
LENGTH: 1123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-436A-285

Query Match 42.5%; Score 54; DB 6; Length 1123;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CCELCNCPAC 18
DB 64 CCAGCCTTGCTGC 76

RESULT 12
US-10-489-448-1704
Sequence 1704, Application US/10489448
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Zhou, Ping
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Ma, Yundqing

APPLICANT: Asundi, Vinod
APPLICANT: Wang, Zhiwei
APPLICANT: Weng, Gezhi
APPLICANT: Haley-Vicente, Dana
APPLICANT: Dmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
CURRENT APPLICATION NUMBER: US/10/489,448
CURRENT FILING DATE: 1004-03-10
PRIOR APPLICATION NUMBER: US 60/324,631
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3476
SOFTWARE: pt FL_genes Version 6.0
SEQ ID NO 1704
LENGTH: 103
TYPE: PRT
ORGANISM: Homo sapiens
US-10-489-448-1704

Query Match 42.1%; Score 53.5; DB 6; Length 103;
Best Local Similarity 61.5%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 6 CCELCNCPACAG 18
Db 45 CCSSCC-PCRCG 56

RESULT 13
US-10-287-436A-258
Sequence 258, Application US/10287436A
GENERAL INFORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RHEUMATOID ARTHRITIS
FILE REFERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 258
LENGTH: 381
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-436A-258

Query Match 41.7%; Score 53; DB 6; Length 381;
Best Local Similarity 66.7%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 CCELCNCPACAG 17

Db 193 CCTACCCACAG 204
RESULT 14
US-10-287-436A-243
Sequence 243, Application US/10287436A
GENERAL INFORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RHEUMATOID ARTHRITIS
FILE REFERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 243
LENGTH: 623
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-436A-243

Query Match 41.7%; Score 53; DB 6; Length 623;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

Qy 6 CCE----LCCNPACAGC 18
Db 366 CCACATCTCTTACAGC 382

RESULT 15
US-10-184-644-525
Sequence 525, Application US/10184644
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Deanovers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4410
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-525
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Query Match      41.7%; Score 53; DB 6; Length 4440;
Best Local Similarity 61.5%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy      6 CCELCNPNACAGC 18
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Db      728 CCTCCCAATAGC 740
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Search completed: March 26, 2005, 17:11:52
Job time : 5.89416 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 26, 2005, 16:39:19 ; Search time 74.365 Seconds
(without alignments)
282.715 Million cell updates/sec

Title: US-10-775-481A-3
Perfect score: 121
Sequence: 1 NTFYCELCCYPACAGCN 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 6959266 seqs, 1168006243 residues
Total number of hits satisfying chosen parameters: 6959266
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
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37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	121	100.0	18	1	PCT-US01-41759A-289	Sequence 289, Appl
2	121	100.0	18	1	PCT-US03-39164A-93	Sequence 93, Appl
3	121	100.0	18	1	PCT-US04-03765-3	Sequence 3, Appl
4	121	100.0	18	1	PCT-US04-05047-80	Sequence 80, Appl
5	121	100.0	18	1	PCT-US94-12232-3	Sequence 3, Appl
6	121	100.0	18	8	US-08-468-449B-3	Sequence 3, Appl
7	121	100.0	18	16	US-09-263-477-3	Sequence 3, Appl
8	121	100.0	18	16	US-09-263-477A-3	Sequence 3, Appl
9	121	100.0	18	21	US-09-724-983-3	Sequence 3, Appl
10	121	100.0	18	24	US-09-930-915A-289	Sequence 289, Appl
11	121	100.0	18	26	US-10-082-014-79	Sequence 79, Appl
12	121	100.0	18	29	US-10-372-076-80	Sequence 80, Appl
13	121	100.0	18	32	US-10-621-684-3	Sequence 3, Appl
14	121	100.0	18	32	US-10-677-074-80	Sequence 80, Appl
15	121	100.0	18	33	US-10-732-862A-93	Sequence 93, Appl
16	121	100.0	18	33	US-10-766-735-3	Sequence 3, Appl
17	121	100.0	18	33	US-10-775-481A-3	Sequence 3, Appl
18	121	100.0	18	33	US-10-796-719-3	Sequence 3, Appl
19	121	100.0	18	34	US-10-805-913-289	Sequence 289, Appl
20	121	100.0	18	34	US-10-806-006-289	Sequence 289, Appl
21	115	95.0	17	1	PCT-US04-03765-23	Sequence 23, Appl
22	115	95.0	17	1	PCT-US94-12232-18	Sequence 18, Appl
23	115	95.0	17	1	PCT-US94-12232-23	Sequence 23, Appl
24	115	95.0	17	8	US-08-468-449B-18	Sequence 18, Appl
25	115	95.0	17	8	US-08-468-449B-23	Sequence 23, Appl
26	115	95.0	17	16	US-09-263-477-18	Sequence 18, Appl
27	115	95.0	17	16	US-09-263-477-23	Sequence 23, Appl
28	115	95.0	17	16	US-09-263-477A-18	Sequence 18, Appl
29	115	95.0	17	16	US-09-263-477A-23	Sequence 23, Appl
30	115	95.0	17	21	US-09-724-983-18	Sequence 18, Appl
31	115	95.0	17	21	US-09-724-983-23	Sequence 23, Appl
32	115	95.0	17	32	US-10-621-684-18	Sequence 18, Appl
33	115	95.0	17	32	US-10-621-684-23	Sequence 23, Appl
34	115	95.0	17	33	US-10-775-481A-23	Sequence 23, Appl
35	110	90.9	16	1	PCT-US04-03765-24	Sequence 24, Appl
36	110	90.9	16	1	PCT-US94-12232-24	Sequence 24, Appl
37	110	90.9	16	8	US-08-468-449B-24	Sequence 24, Appl
38	110	90.9	16	16	US-09-263-477-24	Sequence 24, Appl
39	110	90.9	16	16	US-09-263-477A-24	Sequence 24, Appl
40	110	90.9	16	21	US-09-724-983-24	Sequence 24, Appl
41	110	90.9	16	32	US-10-621-684-24	Sequence 24, Appl
42	110	90.9	16	33	US-10-775-481A-24	Sequence 24, Appl
43	109	90.1	16	1	PCT-US04-03765-19	Sequence 19, Appl
44	109	90.1	16	1	PCT-US94-12232-19	Sequence 19, Appl
45	109	90.1	16	8	US-08-468-449B-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
PCT-US01-41759A-289
; Sequence 289, Application PC/TUS0141759A
; GENERAL INFORMATION: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: PCT/US01/41759A
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: USSN NOT ASSIGNED
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 289

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; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
PCT-US01-41759A-289

Query Match      100.0%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 2
PCT-US03-39164A-93
; Sequence 93, Application PC/TUS0339164A
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, BIRKETT J.
; APPLICANT: LYONS, Katelynne J.
; APPLICANT: JAY, Haron J.
; TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
; FILE REFERENCE: ICG-136.OPCT (4564-91156)
; CURRENT APPLICATION NUMBER: PCT/US03/39164A
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
PCT-US03-39164A-93

Query Match      100.0%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 3
PCT-US04-03765-3
; Sequence 3, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-168 PC1
; CURRENT APPLICATION NUMBER: PCT/US04/03765
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ST I*
PCT-US04-03765-3

Query Match      100.0%; Score 121; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 4
PCT-US04-05047-80
; Sequence 80, Application PC/TUS0405047
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Friebe, Martin
; APPLICANT: Schmidt, Annette Elisabeth
; APPLICANT: Stober, Detlef
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/91569
; CURRENT APPLICATION NUMBER: PCT/US04/05047
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 10/677,074
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 10/372,076
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
PCT-US04-05047-80

Query Match      100.0%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 5
PCT-US94-12232-3
; Sequence 3, Application PC/TUS9412232
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: Compositions That Specifically
; TITLE OF INVENTION: Bind To Colorectal Cancer Cells
; TITLE OF INVENTION: And Methods Of Using The Same
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12232
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,892
; FILING DATE: 26-OCT-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-12232-3

Query Match 100.0%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 6
US-08-468-449B-3
Sequence 3, Application US/08468449B
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds And Methods Of Using The Same
FILE REFERENCE: TJU-1588
CURRENT APPLICATION NUMBER: US/08/468,449B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/141,892
PRIOR FILING DATE: 1993-10-26
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Novel Sequence
US-08-468-449B-3

Query Match 100.0%; Score 121; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 7
US-09-263-477-3
Sequence 3, Application US/09263477
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-263-477-3

Query Match 100.0%; Score 121; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 8
US-09-263-477A-3
Sequence 3, Application US/09263477A
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and
Methods of Using the Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,477A
FILING DATE: 05-Mar-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

;
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-263-477A-3

Query Match 100.0%; Score 121; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 9
US-09-724-983-3

; Sequence 3, Application US/09724983
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
; FILE REFERENCE: TJU-2444
; CURRENT APPLICATION NUMBER: US/09/724,983
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/468,449
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-983-3

Query Match 100.0%; Score 121; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 10

US-09-930-915A-289
; Sequence 289, Application US/09930915A
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,967
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 289
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-930-915A-289

Query Match 100.0%; Score 121; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 11
US-10-082-014-79

; Sequence 79, Application US/10082014
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CYC
; FILE REFERENCE: ICC-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-082-014-79

Query Match 100.0%; Score 121; DB 26; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 12

US-10-372-076-80
; Sequence 80, Application US/10372076
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR CHRONIC HEPATITIS
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-372-076-80

Query Match 100.0%; Score 121; DB 29; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 13

US-10-621-684-3
; Sequence 3, Application US/10621684
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor

CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/621,684
FILING DATE: 17-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/583,447A
FILING DATE: 05-JAN-1996
APPLICATION NUMBER: US 08/141,892
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1702
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-621-684-3

Query Match 100.0%; Score 121; DB 32; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
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Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 14
US-10-677-074-80
; Sequence 80, Application US/10677074
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Friede, Martin
; APPLICANT: Schmidt, Annette Elisabeth
; APPLICANT: Stober, Detlef
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; TITLE OF INVENTION: CHRONIC HEPATITIS
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/677,074
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 10/372,076
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-677-074-80

Query Match 100.0%; Score 121; DB 32; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |
Db 1 NTFYCCCLCCYPACAGCN 18

RESULT 15
US-10-732-862A-93
; Sequence 93, Application US/10732862A
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, BIRKETT J.
; APPLICANT: Lyons, Katelynne J.
; APPLICANT: Jay, Haron J.
; TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
; FILE REFERENCE: ICC-136.0 (4564-88881)
; CURRENT APPLICATION NUMBER: US/10/732,862A
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,123
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/274,616
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-732-862A-93

Query Match 100.0%; Score 121; DB 33; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NTFYCCCLCCYPACAGCN 18
| | | | | | | | | | | | | | | | | |
Db 1 NTFYCCCLCCYPACAGCN 18

Search completed: March 26, 2005, 17:10:16
Job time : 74.365 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2005, 16:44:35 ; Search time 5.58394 Seconds
(without alignments)
187.395 Million cell updates/sec

Title: US-10-775-481A-3

Perfect score: 121

Sequence: 1 NTFYCCBLCCYPACAGCN 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 260697 seqs, 58133403 residues

Total number of hits satisfying chosen parameters: 260697

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
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- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	106	87.6	18	US-10-934-728-24
2	59	48.8	15	US-10-934-728-25
3	59	48.8	15	US-11-066-697-1247
4	59	48.8	15	US-11-066-697-1248
5	58	47.9	3398	1 PCT-US05-03560-6
6	57	47.1	398	6 US-10-450-783-49367
7	54	44.6	381	6 US-10-287-436A-258
8	54	44.6	690	6 US-10-938-061-106
9	54	44.6	690	6 US-10-936-626-106
10	53.5	44.2	103	6 US-10-489-448-1704
11	53	43.8	98	6 US-10-489-448-3215
12	53	43.8	154	6 US-10-489-448-1582
13	53	43.8	463	6 US-10-450-763-58528
14	53	43.8	1071	1 PCT-US05-05406-6
15	53	43.8	1071	7 US-11-060-291-6
16	53	43.8	4440	6 US-10-184-644-525
17	53	43.8	4440	6 US-10-192-007-525
18	52	43.0	1123	6 US-10-287-436A-285
19	52	43.0	1300	6 US-10-184-644-269
20	52	43.0	1300	6 US-10-192-007-269
21	52	43.0	1435	6 US-10-184-644-581
22	52	43.0	1435	6 US-10-192-007-581
23	51.5	42.6	256	6 US-10-450-783-38696
24	51.5	42.6	351	6 US-10-450-763-54057
25	51	42.1	330	6 US-10-287-436A-232

26	51	42.1	623	6	US-10-287-436A-243	Sequence 243, App
27	51	42.1	1894	6	US-10-184-644-97	Sequence 97, Appl
28	51	42.1	1894	6	US-10-192-007-97	Sequence 97, Appl
29	50.5	41.7	400	6	US-10-287-436A-236	Sequence 236, App
30	50.5	41.7	1501	5	US-09-857-581B-16	Sequence 16, Appl
31	50	41.3	12	6	US-10-934-728-22	Sequence 22, Appl
32	50	41.3	16	7	US-11-066-697-1249	Sequence 1249, Ap
33	50	41.3	1200	7	US-11-059-476-3	Sequence 3, Appli
34	49	40.5	109	8	US-60-655-875-164773	Sequence 164773,
35	49	40.5	215	6	US-10-450-763-56787	Sequence 56787, A
36	49	40.5	1743	6	US-10-184-644-451	Sequence 451, App
37	49	40.5	1743	6	US-10-192-007-451	Sequence 451, App
38	48.5	40.1	460	6	US-10-287-436A-274	Sequence 274, App
39	48.5	40.1	508	6	US-10-489-448-1646	Sequence 1646, Ap
40	48.5	40.1	1588	6	US-10-818-210A-2	Sequence 2, Appli
41	48	39.7	12	6	US-10-934-728-23	Sequence 23, Appl
42	48	39.7	21	7	US-11-043-591-231	Sequence 231, App
43	48	39.7	53	6	US-10-450-783-58142	Sequence 58142, A
44	48	39.7	198	1	PCT-US04-42360-567	Sequence 567, App
45	48	39.7	325	7	US-11-043-591-183	Sequence 183, App

ALIGNMENTS

RESULT 1
US-10-934-728-24
; Sequence 24, Application US/10934728
; GENERAL INFORMATION:
; APPLICANT: Balloul, Jean Marc
; APPLICANT: Paul, Stephane
; APPLICANT: Geist, Michel
; APPLICANT: Silvestre, Nathalie
; APPLICANT: Erbs, Philippe
; TITLE OF INVENTION: Poxvirus With Targeted Infection Specificity
; FILE REFERENCE: 032751-115
; CURRENT APPLICATION NUMBER: US/10/934,728
; CURRENT FILING DATE: 2004-09-07
; PRIOR APPLICATION NUMBER: US 09/832,899
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: US 60/246,080
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: EP 0040109.7
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: EP 01440009.7
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sta ligand
US-10-934-728-24

Query Match 87.6%; Score 106; DB 6; Length 18;
Best Local Similarity 94.1%; Pred No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NTFYCCBLCCYPACAGC 17
|||||
Db 1 NTFYCCBLCCNPACAGC 17
|||||

RESULT 2
US-10-934-728-25
; Sequence 25, Application US/10934728
; GENERAL INFORMATION:
; APPLICANT: Balloul, Jean Marc
; APPLICANT: Paul, Stephane
; APPLICANT: Geist, Michel
; APPLICANT: Silvestre, Nathalie

APPLICANT: Erbs, Philippe
; TITLE OF INVENTION: Foxvirus With Targeted Infection Specificity
; FILE REFERENCE: 032751-115
; CURRENT APPLICATION NUMBER: US/10/934,728
; PRIOR FILING DATE: 2004-09-07
; PRIOR APPLICATION NUMBER: US 09/832,899
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: US 60/246,080
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: EP 0040109.7
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: EP 01440009.7
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: endogenous GC-C receptor ligand
US-10-934-728-25

Query Match 48.8%; Score 59; DB 6; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.1;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 CELCCYPACAGC 17
||:|||||
Db 4 CEICAYAACTGC 15

RESULT 3
US-11-066-697-1247
; Sequence 1247, Application US/11066697
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1247
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1247

Query Match 48.8%; Score 59; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.1;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 CELCCYPACAGC 17
||:|||||
Db 4 CEICAYAACTGC 15

RESULT 4
US-11-066-697-1248
; Sequence 1248, Application US/11066697
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1248
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1248

Query Match 48.8%; Score 59; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.1;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 CELCCYPACAGC 17
||:|||||
Db 4 CEICAYAACTGC 15

RESULT 5
PCT-US05-03560-6
; Sequence 6, Application PC/TUS0503560
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: ITPKS AS SMODIFIERS OF THE IGFR PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX05-004C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03560
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,837
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 3398
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-03560-6

Query Match 47.9%; Score 58; DB 1; Length 3398;
Best Local Similarity 61.5%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCELCYPACAGC 17
||:|||||
Db 2463 CCTCCTGTGTCAGC 2475

RESULT 6
US-10-450-763-49367
; Sequence 49367, Application US/10450763
; GENERAL INFORMATION:

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; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CI3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49367
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (170)..(183)
; OTHER INFORMATION: REPEAT PRECURSOR GLYCOPROTEIN EG domain identified by
; OTHER INFORMATION: eMATRIX, accession number PD00120A, p-value=6.727e-11, raw score
; OTHER INFORMATION: 12.94
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(398)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-49367

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Query Match 47.1%; Score 57; DB 6; Length 398;
Best Local Similarity 57.1%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 4 YCCELCCYPACAGC 17
||| ||| ||| |||
Db 232 YCCCCCYYCCCCC 245

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RESULT 7

```

US-10-287-436A-258
; Sequence 258, Application US/10287436A
; GENERAL INFORMATION:

```

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; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-258

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Query Match 44.6%; Score 54; DB 6; Length 381;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 5 CCELCCTCCACAG 16
||| ||| ||| |||
Db 193 CCTACCCACAG 204

```

RESULT 8

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US-10-938-061-106
; Sequence 106, Application US/10938061
; GENERAL INFORMATION:

```

```

; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan

```

```

; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koeppen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; APPLICANT: Sakanaka, Chie
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Reed Chae J.
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1P1B
; CURRENT APPLICATION NUMBER: US/10/938,061
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 10/872,991
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/872,972
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/241,220
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/557,116
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/598,899
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 105
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-061-106

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Query Match 44.6%; Score 54; DB 6; Length 690;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Qy 4 YCCELCCYPACAGC 17
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Db 620 YCCRVCCACCLLC 633

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RESULT 9

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US-10-936-626-106
; Sequence 106, Application US/10936626
; GENERAL INFORMATION:

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; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koeppen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin

```

```

; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1P1
; CURRENT APPLICATION NUMBER: US/10/936,626
; CURRENT FILING DATE: 2004-09-08

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; PRIOR APPLICATION NUMBER: US 10/872,991
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/872,972
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/241,220
; PRIOR FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/557,116
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/598,899
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 106
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-936-626-106

Query Match 44.6%; Score 54; DB 6; Length 690;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 YCCELCYPACAGC 17
||| :|||
Db 620 YCCRVCCACCLLC 633

RESULT 10

US-10-489-448-1704
; Sequence 1704, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yundong
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 3215

; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 1704
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-1704

Query Match 44.2%; Score 53.5; DB 6; Length 103;
Best Local Similarity 61.5%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 5 CCELCYPACAGC 17
||| :|||
Db 45 CCSSCC-PCRGC 56

RESULT 11

US-10-489-448-3215
; Sequence 3215, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yundong
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 3215

; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(98)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for
US-10-489-448-3215

Query Match 43.8%; Score 53; DB 6; Length 98;
Best Local Similarity 70.0%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCELCCTPAC 14
||: |||
Db 16 CCQPCCRPAC 25

RESULT 12
US-10-489-448-1582

; Sequence 1582, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yunqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: Pct_Fl_genes Version 6.0
; SEQ ID NO 1582
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 43.8%; Score 53; DB 6; Length 154;

Best Local Similarity 70.0%; Pred. No. 4.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 5 CCELCCTPAC 14
||: |||
Db 125 CCQPCCRPAC 134

RESULT 13

US-10-450-763-58528
; Sequence 58528, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 58528
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (226)..(235)
; OTHER INFORMATION: Zinc finger C3HC4 type (RING finger), proteins. domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00518, p-value=6.667e-0
; OTHER INFORMATION: raw score of 12.23
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (31)..(148)
; OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name ig,
; OTHER INFORMATION: E-value=0.0072, Pfam score of 14.3
US-10-450-763-58528

Query Match 43.8%; Score 53; DB 6; Length 463;
Best Local Similarity 52.9%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 TFVCCELCCYPACAGCN 18
||: |||
Db 215 TIRCC--CCRRCCGCN 229

RESULT 14

PCT-US05-05406-6
; Sequence 6, Application PC/TUS0505406
; GENERAL INFORMATION:
; APPLICANT: Olsen, Byron
; TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the
; FILE REFERENCE: GTC-223 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/05406
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/545,790
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-05406-6

Query Match 43.8%; Score 53; DB 1; Length 1071;
Best Local Similarity 50.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TFYCCCLCCYPACAGC 17
Db 971 TCCCTGCCCTGCTGC 986

RESULT 15

US-11-060-291-6
; Sequence 6, Application US/11060291
; GENERAL INFORMATION:
; APPLICANT: Olsen, Byron
; TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Useful in the
; FILE REFERENCE: GTC-223
; CURRENT APPLICATION NUMBER: US/11/060,291
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/545,790
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-060-291-6

Query Match 43.8%; Score 53; DB 7; Length 1071;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TFYCCCLCCYPACAGC 17
Db 971 TCCCTGCCCTGCTGC 986

Search completed: March 26, 2005, 17:11:52
Job time : 5.58394 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 26, 2005, 17:44:43 ; Search time 267 Seconds
(without alignments)
498.699 Million cell updates/sec

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Perfect score: 126
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delep 6.0 , Delext 7.0
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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	126	100.0	19	1 PCT-US94-12332-5	Sequence 5, Appli
3	126	100.0	19	8 US-08-468-449B-5	Sequence 5, Appli
4	126	100.0	19	16 US-09-263-477-5	Sequence 5, Appli
5	126	100.0	19	16 US-09-263-477A-5	Sequence 5, Appli
6	126	100.0	19	21 US-09-724-983-5	Sequence 5, Appli
7	126	100.0	19	32 US-10-621-684-5	Sequence 5, Appli
8	126	100.0	19	33 US-10-775-481A-5	Sequence 5, Appli
9	120	95.2	19	1 PCT-US02-09551-23	Sequence 23, Appli
10	120	95.2	19	4 US-08-085-126-20	Sequence 20, Appli
11	120	95.2	19	7 US-08-342-241A-31	Sequence 31, Appli
12	120	95.2	19	8 US-08-438-114-20	Sequence 20, Appli
13	120	95.2	19	16 US-09-291-520-31	Sequence 31, Appli
14	120	95.2	19	16 US-09-525-715-2	Sequence 2, Appli
15	120	95.2	19	27 US-10-107-814-23	Sequence 23, Appli
16	120	95.2	19	29 US-10-371-966-1	Sequence 1, Appli
17	120	95.2	19	30 US-10-479-606-7	Sequence 7, Appli
18	120	95.2	19	33 US-10-766-735-1	Sequence 1, Appli
19	120	95.2	19	33 US-10-766-735-26	Sequence 26, Appli
20	120	95.2	19	33 US-10-796-719-1	Sequence 1, Appli
21	120	95.2	19	33 US-10-796-719-26	Sequence 26, Appli
22	120	95.2	21	33 US-10-766-735-39	Sequence 39, Appli
23	120	95.2	21	33 US-10-766-735-39	Sequence 39, Appli
24	120	95.2	21	33 US-10-796-719-39	Sequence 21, Appli
25	120	95.2	25	33 US-10-766-735-21	Sequence 21, Appli
26	120	95.2	72	33 US-10-796-719-21	Sequence 21, Appli
27	118	93.7	19	33 US-10-766-735-84	Sequence 84, Appli
28	118	93.7	19	33 US-10-766-735-86	Sequence 86, Appli
29	118	93.7	19	33 US-10-796-719-84	Sequence 84, Appli
30	118	93.7	19	33 US-10-796-719-86	Sequence 86, Appli
31	117	92.9	19	33 US-10-766-735-92	Sequence 92, Appli
32	117	92.9	19	33 US-10-796-719-92	Sequence 92, Appli
33	116	92.1	19	29 US-10-371-966-2	Sequence 2, Appli
34	116	92.1	19	33 US-10-766-735-27	Sequence 27, Appli
35	116	92.1	19	33 US-10-766-735-87	Sequence 87, Appli
36	116	92.1	19	33 US-10-796-719-27	Sequence 27, Appli
37	116	92.1	19	33 US-10-796-719-87	Sequence 87, Appli
38	116	92.1	21	33 US-10-766-735-40	Sequence 40, Appli
39	116	92.1	21	33 US-10-766-735-41	Sequence 41, Appli
40	116	92.1	21	33 US-10-796-719-40	Sequence 40, Appli
41	116	92.1	21	33 US-10-796-719-41	Sequence 41, Appli
42	115	91.3	19	33 US-10-766-735-28	Sequence 28, Appli
43	115	91.3	19	33 US-10-766-735-75	Sequence 75, Appli
44	115	91.3	19	33 US-10-766-735-79	Sequence 79, Appli
45	115	91.3	19	33 US-10-766-735-90	Sequence 90, Appli

ALIGNMENTS

RESULT 1
PCT-US04-03765-5
; Sequence 5, Application PC/TUS0403765
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.

APPLICANT: Pitari, Giovanni Mario
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
APPLICANT: Wolfe, Henry R.
APPLICANT: Lubbe, Wilhelm
TITLE OF INVENTION: The Use Of GCC Ligands
FILE REFERENCE: 08321-168 PC1
CURRENT APPLICATION NUMBER: PCT/US04/03765
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 60/446,730
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ST Ib
PCT-US04-03765-5

Alignment Scores:
Pred. No.: 4.98e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x PCT-US04-03765-5 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTGAATGTGTAAATCCTGCTGTAAACGGGTGCTAT 57
|||||
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 2

PCT-US94-12232-5
Sequence 5, Application PC/TUS9412232
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: Compositions That Specifically
TITLE OF INVENTION: Bind To Colorectal Cancer Cells
TITLE OF INVENTION: And Methods Of Using The Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12232
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,892
FILING DATE: 26-OCT-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,056
FILING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1360

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-12232-5

Alignment Scores:
Pred. No.: 4.98e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x PCT-US94-12232-5 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTGAATGTGTAAATCCTGCTGTAAACGGGTGCTAT 57
|||||
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 3

US-08-468-449B-5
Sequence 5, Application US/08468449B
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds And Methods Of Using The Same
FILE REFERENCE: TJU-1598
CURRENT APPLICATION NUMBER: US/08/468,449B
CURRENT FILING DATE: 1993-06-06
PRIOR APPLICATION NUMBER: 08/141,892
PRIOR FILING DATE: 1993-10-26
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Novel Sequence
US-08-468-449B-5

Alignment Scores:
Pred. No.: 4.98e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-468-449B-5 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTGAATGTGTAAATCCTGCTGTAAACGGGTGCTAT 57
|||||
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 4

US-09-263-477-5
Sequence 5, Application US/09263477
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
TITLE OF INVENTION: ST Receptor Binding Compounds and Methods
TITLE OF INVENTION: of Using the Same
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: Pennsylvania

```

; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-263-477A-5

Alignment Scores:
Pred. No.:          4.98e-08      Length:      19
Score:             126.00      Matches:     19
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:       100.00%      Indels:      0
DB:                16          Gaps:        0

US-10-775-481A-4 (1-57) x US-09-263-477A-5 (1-19)

QY 1 AATAGTACAAATTACTGCTGTGAATTGGTTGTTGTAATCTCTGTTGTAACGGGTGCTAT 57
Db 1 AenSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 6
US-09-724-983-5
; Sequence 5, Application US/09724983
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and Methods of Using
; FILE REFERENCE: TJU-2444
; CURRENT APPLICATION NUMBER: US/09/724,983
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/468,449
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-983-5

Alignment Scores:
Pred. No.:          4.98e-08      Length:      19
Score:             126.00      Matches:     19
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:       100.00%      Indels:      0
DB:                21          Gaps:        0

US-10-775-481A-4 (1-57) x US-09-724-983-5 (1-19)

QY 1 AATAGTACAAATTACTGCTGTGAATTGGTTGTTGTAATCTCTGTTGTAACGGGTGCTAT 57
Db 1 AenSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 7
US-10-621-684-5
; Sequence 5, Application US/10621684
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; TITLE OF INVENTION: ST Receptor Binding Compounds and
; Methods of Using the Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor

```

;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: WordPerfect 6.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/621,684
;; FILING DATE: 17-Jul-2003
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/583,447A
;; FILING DATE: 05-JAN-1996
;; APPLICATION NUMBER: US 08/141,892
;; FILING DATE: 26-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeLuca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1702
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;;
;; INFORMATION FOR SEQ ID NO: 5:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-621-684-5

Alignment Scores:
Pred. No.: 4.98e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 32 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-621-684-5 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTAATGCTGTTGTAATCCTGCTTGTAAACGGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 8

US-10-775-481A-5
; Sequence 5, Application US/10775481A
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Pitari, Giovanni Mario
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; APPLICANT: Wolfe, Henry R.
; APPLICANT: Lubbe, Wilhelm
; TITLE OF INVENTION: The Use Of GCC Ligands
; FILE REFERENCE: 08321-0168 US1
; CURRENT APPLICATION NUMBER: US/10/775,481A
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/446,730
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: heat stable toxin peptide Ib
US-10-775-481A-5

Alignment Scores:

Pred. No.: 4.98e-08 Length: 19
Score: 126.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 33 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-775-481A-5 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTAATGCTGTTGTAATCCTGCTTGTAAACGGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysAsnGlyCysTyr 19

RESULT 9

PCT-US02-09551-23
; Sequence 23, Application PC/TUS0209551
; GENERAL INFORMATION:
; APPLICANT: SYNERGY PHARMACEUTICALS
; TITLE OF INVENTION: GUANYLATE CYCLASE RECEPTOR AGONISTS FOR THE TREATMENT
; FILE REFERENCE: 81361/141030
; CURRENT APPLICATION NUMBER: PCT/US02/09551
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (6)..(10)
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (7)..(15)
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (11)..(18)
PCT-US02-09551-23

Alignment Scores:

Pred. No.: 3.26e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 1 Gaps: 0

US-10-775-481A-4 (1-57) x PCT-US02-09551-23 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTAATGCTGTTGTAATCCTGCTTGTAAACGGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 10

US-08-083-126-20
; Sequence 20, Application US/08085126
; GENERAL INFORMATION:
; APPLICANT: LADNER, Robert C.
; APPLICANT: CANNON, Larick E.
; TITLE OF INVENTION: CHELYDRYIMES AND NEPAZYMES, AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 236
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/085,126
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LADNER=10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-085-126-20

Alignment Scores:
Pred. No.: 3.26e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 4 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-085-126-20 (1-19)

Oy 1 AATAGTACCAATTACTGCTGTGAATGCTGTGTAATCTGCTTGAACGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 11
US-08-342-241A-31
Sequence 31, Application US/08342241A
GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
TITLE OF INVENTION: IMMUNOGENS FOR STIMULATING MUCOSAL
TITLE OF INVENTION: IMMUNITY
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,241A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: HOLMG.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176

TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-342-241A-31

Alignment Scores:
Pred. No.: 3.26e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 7 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-342-241A-31 (1-19)

Oy 1 AATAGTACCAATTACTGCTGTGAATGCTGTGTAATCTGCTTGAACGGTGCTAT 57
Db 1 AsnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 12
US-08-438-114-20
Sequence 20, Application US/08438114
GENERAL INFORMATION:
APPLICANT: LADNER, Richard C.
TITLE OF INVENTION: CHELYDRYZYMES AND NEPAZYMES, AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 240
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,114
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,793
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/085,126
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LADNER=10B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-438-114-20

Alignment Scores:

Pred. No.: 3.26e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 8 Gaps: 0

US-10-775-481A-4 (1-57) x US-08-438-114-20 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTAATCTGTTGTAATCTCTGTTGTAACGGGTGCTAT 57
Db 1 AasnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 13

US-09-291-520-31
; Sequence 31, Application US/09291520
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Jan
; APPLICANT: Lebens, Michael
; TITLE OF INVENTION: IMMUNOGENS FOR STIMULATING MUCOSAL
; FILE REFERENCE: HOLMG.001DV1
; CURRENT APPLICATION NUMBER: US/09/291,520A
; CURRENT FILING DATE: 1999-04-04
; EARLIER APPLICATION NUMBER: 08/342,241
; EARLIER FILING DATE: 1994-11-17
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 19
; TYPE: PRT
; ORGANISM: E. coli
US-09-291-520-31

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA: US/09/291,520

FILING DATE:

PRIOR APPLICATION NUMBER: 08/342,241

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: McCormack, Myra H

REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: HOLMG.001A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

TELEX:

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

US-09-291-520-31

Alignment Scores:

Pred. No.: 3.26e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 16 Gaps: 0

US-10-775-481A-4 (1-57) x US-09-291-520-31 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTAATCTGTTGTAATCTCTGTTGTAACGGGTGCTAT 57
Db 1 AasnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 14

US-09-291-520-31
; Sequence 31, Application US/09291520A
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Jan
; APPLICANT: Lebens, Michael
; TITLE OF INVENTION: IMMUNOGENS FOR STIMULATING MUCOSAL
; FILE REFERENCE: HOLMG.001DV1
; CURRENT APPLICATION NUMBER: US/09/291,520A
; CURRENT FILING DATE: 1999-04-04
; EARLIER APPLICATION NUMBER: 08/342,241
; EARLIER FILING DATE: 1994-11-17
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 19
; TYPE: PRT
; ORGANISM: E. coli
US-09-291-520-31

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA: US/09/291,520

FILING DATE:

PRIOR APPLICATION NUMBER: 08/342,241

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: McCormack, Myra H

REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: HOLMG.001A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

TELEX:

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

US-09-291-520-31

Alignment Scores:
Pred. No.: 3.26e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0
DB: 16 Gaps: 0

US-10-775-481A-4 (1-57) x US-09-291-520-31 (1-19)

QY 1 AATAGTAGCAATTACTGCTGTAATCTGTTGTAATCTCTGTTGTAACGGGTGCTAT 57
Db 1 AasnSerSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19

RESULT 15

US-09-525-715-2
; Sequence 2, Application US/09525715
; GENERAL INFORMATION:
; APPLICANT: Johnson, David
; APPLICANT: Losco, Patricia
; APPLICANT: Harris, Mary Ann
; APPLICANT: Hagen, Else Kruger
; APPLICANT: Desai, Vinay
; TITLE OF INVENTION: Transplantable Sarcoma
; FILE REFERENCE: Transplantable Sarcoma-NIDN73110
; CURRENT APPLICATION NUMBER: US/09/525,715
; CURRENT FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/124,437
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: GB9907408.0
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-525-715-2

Alignment Scores:
Pred. No.: 3.26e-07 Length: 19
Score: 120.00 Matches: 18
Percent Similarity: 94.74% Conservative: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 95.24% Indels: 0

DB: 19 Gaps: 0
US-10-775-481A-4 (1-57) x US-09-525-715-2 (1-19)
QY 1 AATAGTAGCAATTACTGCTGTGAATTGTTGTTATCCTGCTTGTAACTGGTGCTAT 57
|||
Db 1 AenSerAsnTyrCysCysGluLeuCysCysAsnProAlaCysThrGlyCysTyr 19
|||

Search completed: March 26, 2005, 18:02:01
Job time : 267 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 26, 2005, 17:47:53 ; Search time 29 Seconds
(without alignments)
228.524 Million cell updates/sec

Title: US-10-775-481A-4
Perfect score: 126
Sequence: 1 aatagtagcaattactgtg.....ctggttgaacgggtgtat 57

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 260697 seqs, 58133403 residues

Total number of hits satisfying chosen parameters: 521394

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool.p/US1075481/runat_25032005_151020_7875/app_query.fasta_1.199
-DB=Pending_Patents_AA_New_QPWT=fastan -SUFFIX=rapn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=DISSIM2 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10775481 @CGN 1 1 23 @runat_25032005_151020_7875 -NCPU=6 -ICPU=3
-NO.MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents AA New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	77.8	18	6	US-10-934-728-24
2	58	46.0	16	7	Sequence 24, Appli
3	56	44.4	282	8	Sequence 1249, Ap
4	55	43.7	98	6	Sequence 128831,
5	55	43.7	154	6	Sequence 3215, Ap
6	54.5	43.3	103	6	Sequence 1582, Ap
7	54	42.9	690	6	Sequence 1704, Ap
8	54	42.9	690	6	Sequence 106, App
9	54	42.9	1071	1	Sequence 106, Appli
10	54	42.9	1071	7	Sequence 6, Appli

11	54	42.9	1123	6	US-10-287-436A-285	Sequence 285, App
12	54	42.9	3398	1	PCT-US05-03560-6	Sequence 6, Appli
c 13	53	51.0	423	8	US-60-643-717-5307	Sequence 5307, Ap
14	52	41.3	152	8	US-60-655-875-169174	Sequence 169174,
15	52	41.3	158	8	US-60-655-875-163386	Sequence 163386,
16	52	41.3	1435	6	US-10-184-644-581	Sequence 581, App
17	52	41.3	1435	6	US-10-192-007-581	Sequence 581, App
18	51	40.5	111	6	US-10-450-763-55164	Sequence 55164, A
19	51	40.5	215	6	US-10-450-763-56787	Sequence 56787, A
20	50.5	40.1	271	8	US-60-655-875-135230	Sequence 135230,
21	50	39.7	15	6	US-10-934-728-25	Sequence 25, Appl
22	50	39.7	15	7	US-11-066-697-1247	Sequence 1247, Ap
23	50	39.7	15	7	US-11-066-697-1248	Sequence 1248, Ap
24	50	39.7	309	1	PCT-US04-17965-1363	Sequence 1363, Ap
25	50	39.7	309	1	PCT-US04-17965B-1363	Sequence 1363, Ap
26	50	39.7	358	8	US-60-655-875-132098	Sequence 132098,
27	50	39.7	424	6	US-10-450-763-42525	Sequence 42525, A
28	50	39.7	508	6	US-10-489-448-1646	Sequence 1646, Ap
29	49.5	39.3	206	6	US-10-450-763-59727	Sequence 59727, A
30	49.5	39.3	1200	7	US-11-058-476-3	Sequence 3, Appli
31	49	38.9	12	6	US-10-934-728-22	Sequence 22, Appl
32	49	38.9	162	8	US-60-655-875-165998	Sequence 165998,
33	49	38.9	264	8	US-60-655-875-137235	Sequence 137235,
34	49	38.9	282	8	US-60-655-875-139718	Sequence 139718,
c 35	49	47.1	399	8	US-60-643-717-12751	Sequence 12751, A
36	49	38.9	857	8	US-60-655-875-153943	Sequence 153943,
37	48.5	38.5	256	6	US-10-450-763-38696	Sequence 38696, A
38	48.5	38.5	351	6	US-10-450-763-54057	Sequence 54057, A
39	48.5	38.5	398	6	US-10-450-763-49367	Sequence 49367, A
40	48.5	38.5	497	6	US-10-287-436A-269	Sequence 269, App
41	48.5	38.5	1501	5	US-09-857-581B-16	Sequence 1392, Ap
42	48	38.1	13	7	US-11-066-697-1392	Sequence 162472,
43	48	38.1	156	8	US-60-655-875-169804	Sequence 169804,
44	48	38.1	181	8	US-60-655-875-169804	Sequence 169804,
45	48	38.1	212	8	US-60-655-875-169914	Sequence 169914,

ALIGNMENTS

RESULT 1
; Sequence 24, Application US/10934728
; GENERAL INFORMATION:
; APPLICANT: Balloul, Jean Marc
; APPLICANT: Geist, Michel
; APPLICANT: Geist, Michel
; APPLICANT: Silvestre, Nathalie
; APPLICANT: Erbs, Philippe
; TITLE OF INVENTION: Poxvirus With Targeted Infection Specificity
; FILE REFERENCE: 032751-115
; CURRENT APPLICATION NUMBER: US/10/934,728
; CURRENT FILING DATE: 2004-09-07
; PRIOR APPLICATION NUMBER: US 09/832,899
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: US 60/246,080
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: EP 0040109.7
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: EP 01440009.7
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sta ligand
US-10-934-728-24
Alignment Scores: 4.39e-07 Length: 18
Pred. No.: 98.00 Matches: 14
Score:

Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 1
Query Match: 77.78% Indels: 0
DB: 6 Gaps: 0

US-10-775-481A-4 (1-57) x US-10-934-728-24 (1-18)

QY 13 TACTGCTGTAATGTGTGTAATCCTGCTGTGTAACGGGTCTAT 57
|||||
Db 4 TyrCysCysGluLeuCysCysAsnProAlaCysAlaGlyCysIyr 18
|||||

RESULT 2

US-11-066-697-1249
; Sequence 1249, Application US/11066697
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1249
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1249

Alignment Scores:
Pred. No.: 0.556 Length: 16
Score: 58.00 Matches: 9
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 3
Query Match: 46.03% Indels: 0
DB: 7 Gaps: 0

US-10-775-481A-4 (1-57) x US-11-066-697-1249 (1-16)

QY 19 TGTGAATGTGTGTAATCCTGCTGTGTAACGGGTGC 54
|||||
Db 4 CysGluLeuCysValAsnValAlaCysThrGlyCys 15
|||||

RESULT 3

US-60-655-875-128831
; Sequence 128831, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF

; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 128831
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_55254; Strand=-; Position=1-18
; OTHER INFORMATION: Homolog annotation: Hit ID=XP_311331.1; Match level="QueryCoverage=100%, HitCoverage=100%, E-value=5e-34, Identity=36%", Hit
; OTHER INFORMATION: description=ENSANGP0000001657 [Anopheles gambiae]
US-60-655-875-128831

Alignment Scores:
Pred. No.: 1.11 Length: 282
Score: 56.00 Matches: 10
Percent Similarity: 63.16% Conservative: 2
Best Local Similarity: 52.63% Mismatches: 5
Query Match: 44.44% Indels: 2
DB: 8 Gaps: 1

US-10-775-481A-4 (1-57) x US-60-655-875-128831 (1-282)

QY 4 AGTAGCAANTACTGCTGT-----GAATTGTTGTAATCCTGCTGTGTAACGGGTGC 54
|||||
Db 239 SerSerAsnHisCysCysThrSerSerCysAsnHisSerSerAsnArgCys 257
|||||

RESULT 4

US-10-489-448-3215
; Sequence 3215, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyao
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yungqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05